

ile 155:MEDLINE(R) 1966-2003/Nov W2

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*File 155: On 13 November, Medline will temporarily stop updating with Completed records. Please see HELP NEWS 154 for details.

Set Items Description

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Cost is in DialUnits

?ds

Set	Items	Description
S1	10402	'SERINE PROTEASES' OR 'SERINE ENDOPEPTIDASES'
S2	37019	R1-R5
S3	332	'ENTEROPEPTIDASE'
S4	14699	E3-E12
S5	11239	E13-E50
S6	2796	E1-E50
S7	76	(S1 OR S2 OR S3) AND (S4 OR S5 OR S6)
S8	43	S7/1997:2003
S9	33	S7 NOT S8
S10	23	S9 AND SERINE?

?e ausp

Ref	Items	Index-term
E1	2	AUSONIA
E2	6	AUSONICS
E3	5	*AUSP
E4	1	AUSPAP
E5	1	AUSPERATE
E6	3	AUSPHARM
E7	1	AUSPICA
E8	1	AUSPICABILE
E9	1	AUSPICABILI
E10	2	AUSPICABLE
E11	1	AUSPICARE
E12	4	AUSPICATE

Enter P or PAGE for more

?s e3

Status: Break Sent.

?e serine protease

Ref	Items	RT	Index-term
E1	0	1	SERINE PHOSPHATE
E2	0	1	SERINE PHOSPHOGLYCERIDES
E3	0		*SERINE PROTEASE
E4	1		SERINE PROTEASE APRM
E5	22		SERINE PROTEASE INHIBITOR 2.1
E6	5		SERINE PROTEASE INHIBITOR 2.3
E7	5		SERINE PROTEASE INHIBITOR 3
E8	0	1	SERINE PROTEASE INHIBITORS
E9	6		SERINE PROTEASE PB92
E10	1		SERINE PROTEASE TESP5, MOUSE
E11	0	1	SERINE PROTEASES
E12	0	1	SERINE PROTEINASE ANTAGONISTS

Enter P or PAGE for more

?p

Ref	Items	RT	Index-term
E13	1		SERINE PROTEINASE INHIBITOR IA-1
E14	1		SERINE PROTEINASE INHIBITOR IA-2
E15	3755	28	SERINE PROTEINASE INHIBITORS
E16	151		SERINE PROTEINASE INHIBITORS --ADMINISTRATION
E17	31		SERINE PROTEINASE INHIBITORS --ADVERSE EFFECTS
E18	127		SERINE PROTEINASE INHIBITORS --ANALYSIS --AN
E19	90		SERINE PROTEINASE INHIBITORS --BIOSYNTHESIS --
E20	155		SERINE PROTEINASE INHIBITORS --BLOOD --BL
E21	243		SERINE PROTEINASE INHIBITORS --CHEMICAL SYNTHESIS
E22	733		SERINE PROTEINASE INHIBITORS --CHEMISTRY --CH
E23	11		SERINE PROTEINASE INHIBITORS --CLASSIFICATION
E24	19		SERINE PROTEINASE INHIBITORS --DEFICIENCY --DF

Enter P or PAGE for more

?e e11

Ref	Items	Type	RT	Index-term
R1	0		1	*SERINE PROTEASES
R2	10402	X	37	SERINE ENDOPEPTIDASES

?s r1 or r2

	0			SERINE PROTEASES
	10402			SERINE ENDOPEPTIDASES
S1	10402			'SERINE PROTEASES' OR 'SERINE ENDOPEPTIDASES'

?e r2

Ref	Items	Type	RT	Index-term
R1	10402		37	*SERINE ENDOPEPTIDASES
R2	10402	X		DC=D8.586.277.656.300.760. (SERINE ENDOPEPTIDASES)
R3	0	X	1	SERINE PROTEASES
R4	0	X	1	SERINE PROTEINASES
R5	37019	B	75	ENDOPEPTIDASES
R6	776	N	3	ACROSIN
R7	432	N	8	ANCROD
R8	468	N	10	ANISTREPLASE
R9	383	N	9	BATROXOBIN
R10	16037	N	3	CHYMOTRYPSIN
R11	1127	N	12	COMPLEMENT FACTOR B
R12	199	N	12	COMPLEMENT FACTOR D

Enter P or PAGE for more

?s r1-r5

	10402			SERINE ENDOPEPTIDASES
	10402			DC=D8.586.277.656.300.760. (SERINE ENDOPEPTIDASES)
	0			SERINE PROTEASES
	0			SERINE PROTEINASES
	37019			ENDOPEPTIDASES
S2	37019			R1-R5

?p

Ref	Items	Type	RT	Index-term
R13	124	N	5	COMPLEMENT FACTOR I
R14	1202	N	3	ENDOPEPTIDASE K
R15	332	N	2	ENTEROPEPTIDASE
R16	371	N	8	FACTOR IXA
R17	1006	N	8	FACTOR VIIA
R18	2328	N	10	FACTOR XA
R19	159	N	8	FACTOR XIA
R20	288	N	8	FACTOR XIIA
R21	6121	N	14	KALLIKREINS
R22	1920	N	6	LEUKOCYTE ELASTASE
R23	6408	N	5	PANCREATIC ELASTASE
R24	23	N	3	PLASMA KALLIKREIN

Enter P or PAGE for more

?s r15

S3 332 'ENTEROPEPTIDASE'

?p

Ref	Items	Type	RT	Index-term
R25	9683	N	4	PLASMIN
R26	5985	N	9	PLASMINOGEN ACTIVATORS
R27	1562	N	7	PREKALLIKREIN
R28	5769	N	4	PRONASE
R29	7745	N	12	PROSTATE-SPECIFIC ANTIGEN
R30	8814	N	8	STREPTOKINASE
R31	2518	N	2	SUBTILISIN
R32	2701	N	3	SUBTILISINS
R33	28692	N	8	THROMBIN
R34	319	N	11	TISSUE KALLIKREINS
R35	9208	N	13	TISSUE PLASMINOGEN ACTIVATOR
R36	54543	N	3	TRYPSIN

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Ref	Items	Type	RT	Index-term
R37	7873	N	10	URINARY PLASMINOGEN ACTIVATOR
R38	0	N	4	VENOMBIN A

?p

>>>Related terms display completed...

?ds

Set	Items	Description
S1	10402	'SERINE PROTEASES' OR 'SERINE ENDOPEPTIDASES'
S2	37019	R1-R5
S3	332	'ENTEROPEPTIDASE'

?e neisseria

Ref	Items	RT	Index-term
E1	1		NEISSEREAL
E2	1		NEISSERI
E3	14699	10	*NEISSERIA
E4	44		NEISSERIA --ANALYSIS --AN
E5	1		NEISSERIA --BLOOD --BL
E6	1		NEISSERIA --CEREBROSPINAL FLUID --CF
E7	15		NEISSERIA --CHEMISTRY --CH
E8	179		NEISSERIA --CLASSIFICATION --CL
E9	27		NEISSERIA --CYTOLOGY --CY
E10	207		NEISSERIA --DRUG EFFECTS --DE
E11	139		NEISSERIA --ENZYMولوجY --EN
E12	155		NEISSERIA --GENETICS --GE

Enter P or PAGE for more

?s e3-e12

14699 NEISSERIA
44 NEISSERIA --ANALYSIS --AN

	1	NEISSERIA	--BLOOD --BL
	1	NEISSERIA	--CEREBROSPINAL FLUID --CF
	15	NEISSERIA	--CHEMISTRY --CH
	179	NEISSERIA	--CLASSIFICATION --CL
	27	NEISSERIA	--CYTOLOGY --CY
	207	NEISSERIA	--DRUG EFFECTS --DE
	139	NEISSERIA	--ENZYMOLGY --EN
	155	NEISSERIA	--GENETICS --GE
S4	14699	E3-E12	

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Ref	Items	RT	Index-term
E13	84		NEISSERIA --GROWTH AND DEVELOPMENT --GD
E14	155		NEISSERIA --IMMUNOLOGY --IM
E15	509		NEISSERIA --ISOLATION AND PURIFICATION --IP
E16	148		NEISSERIA --METABOLISM --ME
E17	125		NEISSERIA --PATHOGENICITY --PY
E18	24		NEISSERIA --PHYSIOLOGY --PH
E19	4		NEISSERIA --RADIATION EFFECTS --RE
E20	11		NEISSERIA --ULTRASTRUCTURE --UL
E21	1		NEISSERIA ADHERENCE-ASSOCIATED PROTEIN, HUMAN
E22	6150	4	NEISSERIA GONORRHOEAE
E23	149		NEISSERIA GONORRHOEAE --ANALYSIS --AN
E24	56		NEISSERIA GONORRHOEAE --CHEMISTRY --CH

Enter P or PAGE for more

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Ref	Items	Index-term
E25	421	NEISSERIA GONORRHOEAE --CLASSIFICATION --CL
E26	71	NEISSERIA GONORRHOEAE --CYTOLOGY --CY
E27	1796	NEISSERIA GONORRHOEAE --DRUG EFFECTS --DE
E28	793	NEISSERIA GONORRHOEAE --ENZYMOLGY --EN
E29	1056	NEISSERIA GONORRHOEAE --GENETICS --GE
E30	480	NEISSERIA GONORRHOEAE --GROWTH AND DEVELOPMENT
E31	836	NEISSERIA GONORRHOEAE --IMMUNOLOGY --IM
E32	1	NEISSERIA GONORRHOEAE --INSTRUMENTATION --IS
E33	2007	NEISSERIA GONORRHOEAE --ISOLATION AND PURIFICA
E34	491	NEISSERIA GONORRHOEAE --METABOLISM --ME
E35	312	NEISSERIA GONORRHOEAE --PATHOGENICITY --PY
E36	197	NEISSERIA GONORRHOEAE --PHYSIOLOGY --PH

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Ref	Items	RT	Index-term
E37	13		NEISSERIA GONORRHOEAE --RADIATION EFFECTS --RE
E38	209		NEISSERIA GONORRHOEAE --ULTRASTRUCTURE --UL
E39	4777	9	NEISSERIA MENINGITIDIS
E40	112		NEISSERIA MENINGITIDIS --ANALYSIS --AN
E41	1		NEISSERIA MENINGITIDIS --CEREBROSPINAL FLUID -
E42	110		NEISSERIA MENINGITIDIS --CHEMISTRY --CH
E43	876		NEISSERIA MENINGITIDIS --CLASSIFICATION --CL
E44	27		NEISSERIA MENINGITIDIS --CYTOLOGY --CY
E45	604		NEISSERIA MENINGITIDIS --DRUG EFFECTS --DE
E46	180		NEISSERIA MENINGITIDIS --ENZYMOLGY --EN
E47	709		NEISSERIA MENINGITIDIS --GENETICS --GE
E48	208		NEISSERIA MENINGITIDIS --GROWTH AND DEVELOPMEN

Enter P or PAGE for more

?s e13-e50

84	NEISSERIA	--GROWTH AND DEVELOPMENT --GD
155	NEISSERIA	--IMMUNOLOGY --IM
509	NEISSERIA	--ISOLATION AND PURIFICATION --IP
148	NEISSERIA	--METABOLISM --ME
125	NEISSERIA	--PATHOGENICITY --PY
24	NEISSERIA	--PHYSIOLOGY --PH
4	NEISSERIA	--RADIATION EFFECTS --RE
11	NEISSERIA	--ULTRASTRUCTURE --UL

1	NEISSERIA ADHERENCE-ASSOCIATED PROTEIN, HUMAN
6150	NEISSERIA GONORRHOEAE
149	NEISSERIA GONORRHOEAE --ANALYSIS --AN
56	NEISSERIA GONORRHOEAE --CHEMISTRY --CH
421	NEISSERIA GONORRHOEAE --CLASSIFICATION --CL
71	NEISSERIA GONORRHOEAE --CYTOLOGY --CY
1796	NEISSERIA GONORRHOEAE --DRUG EFFECTS --DE
793	NEISSERIA GONORRHOEAE --ENZYMOLGY --EN
1056	NEISSERIA GONORRHOEAE --GENETICS --GE
480	NEISSERIA GONORRHOEAE --GROWTH AND DEVELOPMENT
836	NEISSERIA GONORRHOEAE --IMMUNOLOGY --IM
1	NEISSERIA GONORRHOEAE --INSTRUMENTATION --IS
2007	NEISSERIA GONORRHOEAE --ISOLATION AND PURIFICA
491	NEISSERIA GONORRHOEAE --METABOLISM --ME
312	NEISSERIA GONORRHOEAE --PATHOGENICITY --PY
197	NEISSERIA GONORRHOEAE --PHYSIOLOGY --PH
13	NEISSERIA GONORRHOEAE --RADIATION EFFECTS --RE
209	NEISSERIA GONORRHOEAE --ULTRASTRUCTURE --UL
4777	NEISSERIA MENINGITIDIS
112	NEISSERIA MENINGITIDIS --ANALYSIS --AN
1	NEISSERIA MENINGITIDIS --CEREBROSPINAL FLUID -
110	NEISSERIA MENINGITIDIS --CHEMISTRY --CH
876	NEISSERIA MENINGITIDIS --CLASSIFICATION --CL
27	NEISSERIA MENINGITIDIS --CYTOLOGY --CY
604	NEISSERIA MENINGITIDIS --DRUG EFFECTS --DE
180	NEISSERIA MENINGITIDIS --ENZYMOLGY --EN
709	NEISSERIA MENINGITIDIS --GENETICS --GE
208	NEISSERIA MENINGITIDIS --GROWTH AND DEVELOPMEN
1658	NEISSERIA MENINGITIDIS --IMMUNOLOGY --IM
1307	NEISSERIA MENINGITIDIS --ISOLATION AND PURIFIC
S5 11239	E13-E50

?p

Ref	Items	Index-term
E49	1658	NEISSERIA MENINGITIDIS --IMMUNOLOGY --IM
E50	1307	NEISSERIA MENINGITIDIS --ISOLATION AND PURIFIC

?p

Ref	Items	RT	Index-term
E1	1307		NEISSERIA MENINGITIDIS --ISOLATION AND PURIFIC
E2	310		NEISSERIA MENINGITIDIS --METABOLISM --ME
E3	348		NEISSERIA MENINGITIDIS --PATHOGENICITY --PY
E4	109		NEISSERIA MENINGITIDIS --PHYSIOLOGY --PH
E5	3		NEISSERIA MENINGITIDIS --RADIATION EFFECTS --R
E6	90		NEISSERIA MENINGITIDIS --ULTRASTRUCTURE --UL
E7	4		NEISSERIA MENINGITIDIS --VIROLOGY --VI
E8	9	4	NEISSERIA MENINGITIDIS, SEROGROUP A
E9	1		NEISSERIA MENINGITIDIS, SEROGROUP A --CLASSIFI
E10	2		NEISSERIA MENINGITIDIS, SEROGROUP A --GENETICS
E11	7		NEISSERIA MENINGITIDIS, SEROGROUP A --IMMUNOLO
E12	2		NEISSERIA MENINGITIDIS, SEROGROUP A --ISOLATIO

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Ref	Items	RT	Index-term
E13	1		NEISSERIA MENINGITIDIS, SEROGROUP A --PATHOGEN
E14	21	4	NEISSERIA MENINGITIDIS, SEROGROUP B
E15	1		NEISSERIA MENINGITIDIS, SEROGROUP B --ENZYMOL
E16	7		NEISSERIA MENINGITIDIS, SEROGROUP B --GENETICS
E17	1		NEISSERIA MENINGITIDIS, SEROGROUP B --GROWTH A
E18	14		NEISSERIA MENINGITIDIS, SEROGROUP B --IMMUNOLO
E19	4		NEISSERIA MENINGITIDIS, SEROGROUP B --ISOLATIO
E20	2		NEISSERIA MENINGITIDIS, SEROGROUP B --METABOLI
E21	6		NEISSERIA MENINGITIDIS, SEROGROUP B --PATHOGEN
E22	34	4	NEISSERIA MENINGITIDIS, SEROGROUP C
E23	1		NEISSERIA MENINGITIDIS, SEROGROUP C --CLASSIFI
E24	1		NEISSERIA MENINGITIDIS, SEROGROUP C --ENZYMOL

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Ref	Items	RT	Index-term
E25	4		NEISSERIA MENINGITIDIS, SEROGROUP C --GENETICS
E26	1		NEISSERIA MENINGITIDIS, SEROGROUP C --GROWTH A
E27	15		NEISSERIA MENINGITIDIS, SEROGROUP C --IMMUNOLO
E28	11		NEISSERIA MENINGITIDIS, SEROGROUP C --ISOLATIO
E29	2		NEISSERIA MENINGITIDIS, SEROGROUP C --METABOLI
E30	4		NEISSERIA MENINGITIDIS, SEROGROUP C --PATHOGEN
E31	9	3	NEISSERIA MENINGITIDIS, SEROGROUP W-135
E32	3		NEISSERIA MENINGITIDIS, SEROGROUP W-135 --CLAS
E33	2		NEISSERIA MENINGITIDIS, SEROGROUP W-135 --GENE
E34	2		NEISSERIA MENINGITIDIS, SEROGROUP W-135 --IMMU
E35	6		NEISSERIA MENINGITIDIS, SEROGROUP W-135 --ISOL
E36	4	4	NEISSERIA MENINGITIDIS, SEROGROUP Y

Enter P or PAGE for more

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Ref	Items	RT	Index-term
E37	2		NEISSERIA MENINGITIDIS, SEROGROUP Y --CLASSIFI
E38	1		NEISSERIA MENINGITIDIS, SEROGROUP Y --DRUG EFF
E39	1		NEISSERIA MENINGITIDIS, SEROGROUP Y --ENZYMOL
E40	2		NEISSERIA MENINGITIDIS, SEROGROUP Y --GENETICS
E41	2		NEISSERIA MENINGITIDIS, SEROGROUP Y --ISOLATIO
E42	788	19	NEISSERIAACEAE
E43	8		NEISSERIAACEAE --ANALYSIS --AN
E44	3		NEISSERIAACEAE --CHEMISTRY --CH
E45	46		NEISSERIAACEAE --CLASSIFICATION --CL
E46	1		NEISSERIAACEAE --CYTOLOGY --CY
E47	58		NEISSERIAACEAE --DRUG EFFECTS --DE
E48	45		NEISSERIAACEAE --ENZYMOLGY --EN

Enter P or PAGE for more

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Ref	Items	Index-term
E49	21	NEISSERIAACEAE --GENETICS --GE
E50	10	NEISSERIAACEAE --GROWTH AND DEVELOPMENT --GD

?s e1-e50

1307	NEISSERIA MENINGITIDIS --ISOLATION AND PURIFIC
310	NEISSERIA MENINGITIDIS --METABOLISM --ME
348	NEISSERIA MENINGITIDIS --PATHOGENICITY --PY
109	NEISSERIA MENINGITIDIS --PHYSIOLOGY --PH
3	NEISSERIA MENINGITIDIS --RADIATION EFFECTS --R
90	NEISSERIA MENINGITIDIS --ULTRASTRUCTURE --UL
4	NEISSERIA MENINGITIDIS --VIROLOGY --VI
9	NEISSERIA MENINGITIDIS, SEROGROUP A
1	NEISSERIA MENINGITIDIS, SEROGROUP A --CLASSIFI
2	NEISSERIA MENINGITIDIS, SEROGROUP A --GENETICS
7	NEISSERIA MENINGITIDIS, SEROGROUP A --IMMUNOLO
2	NEISSERIA MENINGITIDIS, SEROGROUP A --ISOLATIO
1	NEISSERIA MENINGITIDIS, SEROGROUP A --PATHOGEN
21	NEISSERIA MENINGITIDIS, SEROGROUP B
1	NEISSERIA MENINGITIDIS, SEROGROUP B --ENZYMOL
7	NEISSERIA MENINGITIDIS, SEROGROUP B --GENETICS
1	NEISSERIA MENINGITIDIS, SEROGROUP B --GROWTH A
14	NEISSERIA MENINGITIDIS, SEROGROUP B --IMMUNOLO
4	NEISSERIA MENINGITIDIS, SEROGROUP B --ISOLATIO
2	NEISSERIA MENINGITIDIS, SEROGROUP B --METABOLI
6	NEISSERIA MENINGITIDIS, SEROGROUP B --PATHOGEN
34	NEISSERIA MENINGITIDIS, SEROGROUP C
1	NEISSERIA MENINGITIDIS, SEROGROUP C --CLASSIFI
1	NEISSERIA MENINGITIDIS, SEROGROUP C --ENZYMOL
4	NEISSERIA MENINGITIDIS, SEROGROUP C --GENETICS
1	NEISSERIA MENINGITIDIS, SEROGROUP C --GROWTH A
15	NEISSERIA MENINGITIDIS, SEROGROUP C --IMMUNOLO
11	NEISSERIA MENINGITIDIS, SEROGROUP C --ISOLATIO

2 NEISSERIA MENINGITIDIS, SEROGROUP C --METABOLI
 4 NEISSERIA MENINGITIDIS, SEROGROUP C --PATHOGEN
 9 NEISSERIA MENINGITIDIS, SEROGROUP W-135
 3 NEISSERIA MENINGITIDIS, SEROGROUP W-135 --CLAS
 2 NEISSERIA MENINGITIDIS, SEROGROUP W-135 --GENE
 2 NEISSERIA MENINGITIDIS, SEROGROUP W-135 --IMMU
 6 NEISSERIA MENINGITIDIS, SEROGROUP W-135 --ISOL
 4 NEISSERIA MENINGITIDIS, SEROGROUP Y
 2 NEISSERIA MENINGITIDIS, SEROGROUP Y --CLASSIFI
 1 NEISSERIA MENINGITIDIS, SEROGROUP Y --DRUG EFF
 1 NEISSERIA MENINGITIDIS, SEROGROUP Y --ENZYMOL
 2 NEISSERIA MENINGITIDIS, SEROGROUP Y --GENETICS
 2 NEISSERIA MENINGITIDIS, SEROGROUP Y --ISOLATIO
 788 NEISSERIAACEAE
 8 NEISSERIAACEAE --ANALYSIS --AN
 3 NEISSERIAACEAE --CHEMISTRY --CH
 46 NEISSERIAACEAE --CLASSIFICATION --CL
 1 NEISSERIAACEAE --CYTOLOGY --CY
 58 NEISSERIAACEAE --DRUG EFFECTS --DE
 45 NEISSERIAACEAE --ENZYMOLGY --EN
 21 NEISSERIAACEAE --GENETICS --GE
 10 NEISSERIAACEAE --GROWTH AND DEVELOPMENT --GD
 S6 2796 E1-E50

?ds

Set	Items	Description
S1	10402	'SERINE PROTEASES' OR 'SERINE ENDOPEPTIDASES'
S2	37019	R1-R5
S3	332	'ENTEROPEPTIDASE'
S4	14699	E3-E12
S5	11239	E13-E50
S6	2796	E1-E50

?s (s1 or s2 or s3) and (s4 or s5 or s6)

10402 S1
 37019 S2
 332 S3
 14699 S4
 11239 S5
 2796 S6

S7 76 (S1 OR S2 OR S3) AND (S4 OR S5 OR S6)

?s s7/1997:2003

76 S7
 3305438 PY=1997 : PY=2003

S8 43 S7/1997:2003

?s s7 not s8

76 S7
 43 S8
 S9 33 S7 NOT S8

?t s9/9/all

9/9/1

DIALOG(R) File 155:MEDLINE(R)

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10797128 97086622 PMID: 8932311

Characterization of EspC, a 110-kilodalton protein secreted by enteropathogenic Escherichia coli which is homologous to members of the immunoglobulin A protease-like family of secreted proteins.

Stein M; Kenny B; Stein M A; Finlay B B

Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, Canada.

Journal of bacteriology (UNITED STATES) Nov 1996, 178 (22) p6546-54,

ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Enteropathogenic Escherichia coli (EPEC) secretes at least five proteins.

Two of these proteins, EspA and EspB (previously called EaeB), activate signal transduction pathways in host epithelial cells. While the role of the other three proteins (39, 40, and 110 kDa) remains undetermined, secretion of all five proteins is under the control of perA, a known positive regulator of several EPEC virulence factors. On the basis of amino-terminal protein sequence data, we cloned and sequenced the gene which encodes the 110-kDa secreted protein and examined its possible role in EPEC signaling and interaction with epithelial cells. In accordance with the terminology used for espA and espB, we called this gene espC, for EPEC-secreted protein C. We found significant homology between the predicted EspC protein sequence and a family of immunoglobulin A (IgA) protease-like proteins which are widespread among pathogenic bacteria. Members of this protein family are found in avian pathogenic *Escherichia coli* (Tsh), *Haemophilus influenzae* (Hap), and *Shigella flexneri* (SepA). Although these proteins and EspC do not encode IgA protease activity, they have considerable homology with IgA protease from *Neisseria gonorrhoeae* and *H. influenzae* and appear to use a export system for secretion. We found that genes homologous to espC also exist in other pathogenic bacteria which cause attaching and effacing lesions, including *Hafnia alvei* biotype 19982, *Citrobacter freundii* biotype 4280, and rabbit diarrheagenic *E. coli* (RDEC-1). Although these strains secrete various proteins similar in molecular size to the proteins secreted by EPEC, we did not detect secretion of a 110-kDa protein by these strains. To examine the possible role of EspC in EPEC interactions with epithelial cells, we constructed a deletion mutant in espC by allelic exchange and characterized the mutant by standard tissue culture assays. We found that EspC is not necessary for mediating EPEC-induced signal transduction in HeLa epithelial cells and does not play a role in adherence or invasion of tissue culture cells.

Tags: Comparative Study; Human; Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--secretion--SE; **Escherichia coli* --genetics--GE; **Escherichia coli*--pathogenicity--PY; *Genes, Structural, Bacterial; *Intestines--microbiology--MI; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Bacterial Proteins--metabolism--ME; Caco-2 Cells; Cell Communication; Chromosomes, Bacterial; Cloning, Molecular; Databases, Factual; Enterobacteriaceae--genetics--GE; Enterobacteriaceae--pathogenicity--PY; Epithelium--microbiology--MI; Epithelium--pathology--PA; *Escherichia coli*--enzymology--EN; HeLa Cells; Molecular Sequence Data; Mutation; Sequence Analysis, DNA; Sequence Homology, Amino Acid; **Serine Endopeptidases --genetics --GE; Species Specificity**

Molecular Sequence Databank No.: GENBANK/U69128

CAS Registry No.: 0 (Bacterial Proteins); 0 (EspC protein)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19970107

Record Date Completed: 19970107

9/9/2

DIALOG(R) File 155:MEDLINE(R)

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10791088 97080554 PMID: 8921899

Absence of periplasmic DsbA oxidoreductase facilitates export of cysteine-containing passenger proteins to the *Escherichia coli* cell surface via the IgA beta autotransporter pathway.

Jose J; Kramer J; Klauser T; Pohlner J; Meyer T F

Max-Planck-Institut fur Biologie, Abteilung Infektionsbiologie, Tübingen, Germany.

Gene (NETHERLANDS) Oct 31 1996, 178 (1-2) p107-10, ISSN 0378-1119
Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The IgA beta autotransporter function of IgA1 protease from *Neisseria gonorrhoeae* was assessed in *Escherichia coli* using the *Vibrio cholerae* toxin B subunit (CtxB) as a heterologous passenger. N-terminal fusions with IgA beta of native CtxB or mutant CtxB protein containing no cysteines were

constructed and analysed in isogenic E. coli mutants carrying defects in either or both the ompT (outer membrane protease T) and dsbA (periplasmic disulfide oxidoreductase) determinants. While export of the cysteine-less CtxB passenger was independent of the dsbA genotype, the native CtxB passenger was properly translocated across the outer membrane only in the dsbA mutant background. This effect was consistent in the presence and in the absence of the OmpT protease which rather determined the release of surface-bound CtxB into the medium. Therefore, in agreement with previous observations Iga beta-dependent protein secretion requires an unfolded conformation of the passenger domain and can be blocked by disulfide loop formation in the presence of DsbA. Since DsbA acts in the periplasm, this provides evidence for a periplasmic intermediate in the Iga beta-mediated export pathway. E. coli (dsbA ompT) is highly suitable as a strain for the surface display of recombinant proteins via Iga beta, whether or not they contain cysteine residues.

Tags: Support, Non-U.S. Gov't

Descriptors: Cysteine--metabolism--ME; *Escherichia coli--metabolism--ME; *Isomerases--metabolism--ME; *Oxidoreductases--metabolism--ME; * **Serine Endopeptidases** --metabolism --ME; Biological Transport; Cell Membrane --metabolism--ME; Cholera Toxin--genetics--GE; Cholera Toxin--metabolism --ME; Escherichia coli--enzymology--EN; Escherichia coli--genetics--GE; Isomerases--genetics--GE; Molecular Sequence Data; Mutation; Oxidoreductases--genetics--GE; Protein Disulfide-Isomerase; Recombinant Fusion Proteins--genetics--GE; Recombinant Fusion Proteins--metabolism--ME ; Recombinant Fusion Proteins--secretion--SE; **Serine Endopeptidases --genetics** --GE; Vibrio cholerae--genetics--GE

Molecular Sequence Databank No.: GENBANK/X80762

CAS Registry No.: 0 (Recombinant Fusion Proteins); 52-90-4 (Cysteine); 9012-63-9 (Cholera Toxin)

Enzyme No.: EC 1. (Oxidoreductases); EC 1.8.4.- (periplasmic protein disulfide oxidoreductase); EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (Iga-specific serine endopeptidase); EC 3.4.21.87 (omptin); EC 5. (Isomerases); EC 5.3.4.1 (Protein Disulfide-Isomerase)

Record Date Created: 19961231

Record Date Completed: 19961231

9/9/3

DIALOG(R) File 155:MEDLINE(R)

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10737128 97086622 PMID: 8932311

Characterization of EspC, a 110-kilodalton protein secreted by enteropathogenic Escherichia coli which is homologous to members of the immunoglobulin A protease-like family of secreted proteins.

Stein M; Kenny B; Stein M A; Finlay B B

Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, Canada.

Journal of bacteriology (UNITED STATES) Nov 1996, 178 (22) p6546-54, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Enteropathogenic Escherichia coli (EPEC) secretes at least five proteins. Two of these proteins, EspA and EspB (previously called EaeB), activate signal transduction pathways in host epithelial cells. While the role of the other three proteins (39, 40, and 110 kDa) remains undetermined, secretion of all five proteins is under the control of perA, a known positive regulator of several EPEC virulence factors. On the basis of amino-terminal protein sequence data, we cloned and sequenced the gene which encodes the 110-kDa secreted protein and examined its possible role in EPEC signaling and interaction with epithelial cells. In accordance with the terminology used for espA and espB, we called this gene espC, for EPEC-secreted protein C. We found significant homology between the predicted EspC protein sequence and a family of immunoglobulin A (IgA) protease-like proteins which are widespread among pathogenic bacteria. Members of this protein family are found in avian pathogenic Escherichia

coli (Tsh), Haemophilus influenzae (Hap), and Shigella flexneri (SepA). Although these proteins and EspC do not encode IgA protease activity, they have considerable homology with IgA protease from *Neisseria gonorrhoeae* and *H. influenzae* and appear to use a export system for secretion. We found that genes homologous to espC also exist in other pathogenic bacteria which cause attaching and effacing lesions, including *Hafnia alvei* biotype 19982, *Citrobacter freundii* biotype 4280, and rabbit diarrheagenic *E. coli* (RDEC-1). Although these strains secrete various proteins similar in molecular size to the proteins secreted by EPEC, we did not detect secretion of a 110-kDa protein by these strains. To examine the possible role of EspC in EPEC interactions with epithelial cells, we constructed a deletion mutant in espC by allelic exchange and characterized the mutant by standard tissue culture assays. We found that EspC is not necessary for mediating EPEC-induced signal transduction in HeLa epithelial cells and does not play a role in adherence or invasion of tissue culture cells.

Tags: Comparative Study; Human; Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--secretion--SE; *Escherichia coli--genetics--GE; *Escherichia coli--pathogenicity--PY; *Genes, Structural, Bacterial; *Intestines--microbiology--MI; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Bacterial Proteins--metabolism--ME; Caco-2 Cells; Cell Communication; Chromosomes, Bacterial; Cloning, Molecular; Databases, Factual; Enterobacteriaceae--genetics--GE; Enterobacteriaceae--pathogenicity--PY; Epithelium--microbiology--MI; Epithelium--pathology--PA; Escherichia coli--enzymology--EN; HeLa Cells; Molecular Sequence Data; Mutation; Sequence Analysis, DNA; Sequence Homology, Amino Acid; Serine-Endopeptidases --genetics --GE; Species Specificity

Molecular Sequence Databank No.: GENBANK/U69128

CAS Registry No.: 0 (Bacterial Proteins); 0 (EspC protein)

Enzyme No.: EC 3.4.21 (Serine Endopeptidases); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19970107

Record Date Completed: 19970107

9/9/4

DIALOG(R) File 155:MEDLINE(R)

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10731088 97080554 PMID: 8921899

Absence of periplasmic DsbA oxidoreductase facilitates export of cysteine-containing passenger proteins to the Escherichia coli cell surface via the Iga beta autotransporter pathway.

Jose J; Kramer J; Klauser T; Pohlner J; Meyer T F

Max-Planck-Institut fur Biologie, Abteilung Infektionsbiologie, Tubingen, Germany.

Gene (NETHERLANDS) Oct 31 1996, 178 (1-2) p107-10, ISSN 0378-1119
Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The Iga beta autotransporter function of IgA1 protease from *Neisseria gonorrhoeae* was assessed in *Escherichia coli* using the *Vibrio cholerae* toxin B subunit (CtxB) as a heterologous passenger. N-terminal fusions with Iga beta of native CtxB or mutant CtxB protein containing no cysteines were constructed and analysed in isogenic *E. coli* mutants carrying defects in either or both the ompT (outer membrane protease T) and dsbA (periplasmic disulfide oxidoreductase) determinants. While export of the cysteine-less CtxB passenger was independent of the dsbA genotype, the native CtxB passenger was properly translocated across the outer membrane only in the dsbA mutant background. This effect was consistent in the presence and in the absence of the OmpT protease which rather determined the release of surface-bound CtxB into the medium. Therefore, in agreement with previous observations Iga beta-dependent protein secretion requires an unfolded conformation of the passenger domain and can be blocked by disulfide loop formation in the presence of DsbA. Since DsbA acts in the periplasm, this provides evidence for a periplasmic intermediate in the Iga beta-mediated export pathway. *E. coli* (dsbA ompT) is highly suitable as a strain for the

surface display of recombinant proteins via Iga beta, whether or not they contain cysteine residues.

Tags: Support, Non-U.S. Gov't

Descriptors: Cysteine--metabolism--ME; *Escherichia coli--metabolism--ME; *Isomerases--metabolism--ME; *Oxidoreductases--metabolism--ME; * **Serine Endopeptidases** --metabolism --ME; Biological Transport; Cell Membrane --metabolism--ME; Cholera Toxin--genetics--GE; Cholera Toxin--metabolism --ME; Escherichia coli--enzymology--EN; Escherichia coli--genetics--GE; Isomerases--genetics--GE; Molecular Sequence Data; Mutation; Oxidoreductases--genetics--GE; Protein Disulfide-Isomerase; Recombinant Fusion Proteins--genetics--GE; Recombinant Fusion Proteins--metabolism--ME; Recombinant Fusion Proteins--secretion--SE; **Serine Endopeptidases** --genetics --GE; Vibrio cholerae--genetics--GE

Molecular Sequence Databank No.: GENBANK/X80762

CAS Registry No.: 0 (Recombinant Fusion Proteins); 52-90-4 (Cysteine); 9012-63-9 (Cholera Toxin)

Enzyme No.: EC 1. (Oxidoreductases); EC 1.8.4.- (periplasmic protein disulfide oxidoreductase); EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (Iga-specific serine endopeptidase); EC 3.4.21.87 (omptin); EC 5. (Isomerases); EC 5.3.4.1 (Protein Disulfide-Isomerase)

Record Date Created: 19961231

Record Date Completed: 19961231

9/9/5

DIALOG(R) File 155:MEDLINE(R)

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10706086 97055419 PMID: 8899706

Processing of the AIDA-I precursor: removal of AIDAc and evidence for the outer membrane anchoring as a beta-barrel structure.

Suhr M; Benz I; Schmidt M A

Institut fur Infektiologie, Zentrum fur Molekularbiologie, Entzundung (ZMBE), Munster, Germany.

Molecular microbiology (ENGLAND) Oct 1996, 22 (1) p31-42, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The AIDA-I adhesin known to be responsible for the diffuse adherence (DA) phenotype of the diarrhoeagenic Escherichia coli (DAEC) strain 2787 has been shown previously to be synthesized as a precursor protein and to undergo additional C-terminal processing. Here, the C-terminal processing of the AIDA-I precursor and the outer membrane topology of the cleaved C-terminal fragment, AIDAc, were investigated. By isolation of the cleaved AIDAc fragment and N-terminal sequencing, the C-terminal cleavage site was identified between Ser-846 and Ala-847 thereby indicating a molecular mass of 47.5 kDa for AIDAc. The correct processing to AIDA-I and AIDAc in OmpT, OmpP and DegP protease-deficient E. coli strains as well as in avirulent salmonellae and shigellae points to an autocatalytic cleavage mechanism. The cleaved AIDAc was localized in the outer membrane. A leader sequence-AIDAc fusion was efficiently routed to the outer membrane. Analysis by protease digestion, secondary-structure prediction and modelling, by comparison with structurally related bacterial proteins like the IgA1 protease from *neisseria*, the vacuolating toxin from Helicobacter pylori, and the VirG protein of Shigella flexneri, strongly indicates that AIDAc is present in the outer membrane as a beta-barrel structure.

Descriptors: *Adhesins, Escherichia coli--biosynthesis--BI; *Escherichia coli--metabolism--ME; *Protein Precursors--metabolism--ME; *Protein Processing, Post-Translational; *Protein Structure, Secondary; Adhesins, Escherichia coli--chemistry--CH; Adhesins, Escherichia coli--immunology --IM; Amino Acid Sequence; Antibodies, Bacterial; Blotting, Western; Cell Compartmentation; Cell Membrane--ultrastructure--UL; **Endopeptidases** --deficiency--DF; **Endopeptidases** --metabolism--ME; Escherichia coli --genetics--GE; Molecular Sequence Data; Protein Precursors--chemistry--CH; Protein Precursors--immunology--IM; Sequence Analysis

Molecular Sequence Databank No.: GENBANK/X65022

CAS Registry No.: 0 (AIDA-I protein); 0 (Adhesins, Escherichia coli);
0 (Antibodies, Bacterial); 0 (Protein Precursors)
Enzyme No.: EC 3.4.- (**Endopeptidases**)
Record Date Created: 19970219
Record Date Completed: 19970219

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DIALOG(R) File 155:MEDLINE(R)

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10600311 96417863 PMID: 8820654

Cloning of an Aeromonas hydrophila type IV pilus biogenesis gene cluster: complementation of pilus assembly functions and characterization of a type IV leader peptidase/N-methyltransferase required for extracellular protein secretion.

Pepe C M; Eklund M W; Strom M S

US Department of Commerce, NOAA, Seattle, Washington 98112-2097, USA.

Molecular microbiology (ENGLAND) Feb 1996, 19 (4) p857-69, ISSN
0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Aeromonas hydrophila secretes several extracellular proteins that are associated with virulence including an enterotoxin, a protease, and the hole-forming toxin, aerolysin. These degradative enzymes and toxins are exported by a conserved pathway found in many Gram-negative bacteria. In *Pseudomonas aeruginosa* this export pathway and type IV pilus biogenesis are dependent on the product of the *pilD* gene. *PilD* is a bifunctional enzyme that processes components of the extracellular secretory pathway as well as a type IV prepilin. An *A. hydrophila* genomic library was transferred into a *P. aeruginosa pilD* mutant that is defective for type IV pilus biogenesis. The *A. hydrophila pilD* homologue, *tapD*, was identified by its ability to complement the *pilD* mutation in *P. aeruginosa*. Transconjugants containing *tapD* were sensitive to the type IV pilus-specific phage, P04. Sequence data revealed that *tapD* is part of a cluster of genes (*tapABCD*) that are homologous to *P. aeruginosa* type IV pilus biogenesis genes (*pilABCD*). We showed that *TapB* and *TapC* are functionally homologous to *P. aeruginosa PilB* and *PilC*, the first such functional complementation of pilus assembly demonstrated between bacteria that express type IV pili. In vitro studies revealed that *TapD* has both endopeptidase and N-methyltransferase activities using *P. aeruginosa* prepilin as substrate. Furthermore, we show that *tapD* is required for extracellular secretion of aerolysin and protease, indicating that *tapD* may play an important role in the virulence of *A. hydrophila*.

Tags: Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Aeromonas hydrophila*--genetics--GE; *Bacterial Proteins
--secretion--SE; * **Endopeptidases** --genetics--GE; *Fimbriae, Bacterial
--genetics--GE; *Genes, Bacterial; *Methyltransferases--genetics--GE;
*Multienzyme Complexes--genetics--GE; Amino Acid Sequence; Bacterial
Proteins--genetics--GE; Bacterial Toxins--metabolism--ME; Base Sequence;
Cloning, Molecular; Genetic Complementation Test; Molecular Sequence Data;
Multigene Family; Mutation; Sequence Analysis, DNA; Sequence Homology,
Amino Acid

Molecular Sequence Databank No.: GENBANK/U20255

CAS Registry No.: 0 (Bacterial Proteins); 0 (Bacterial Toxins); 0
(Multienzyme Complexes); 0 (*PilD* protein); 0 (*pilC* protein, *Neisseria*
gonorrhoeae); 122319-68-0 (*pilB* protein); 53126-24-2 (aerolysin)

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 3.4.- (**Endopeptidases**
); EC 3.4.99.- (*TapD* protein)

Record Date Created: 19961216

Record Date Completed: 19961216

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DIALOG(R) File 155:MEDLINE(R)

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10491810 96302316 PMID: 8703438

Biological significance of IgA1 proteases in bacterial colonization and pathogenesis: critical evaluation of experimental evidence.

Kilian M; Reinholdt J; Lomholt H; Poulsen K; Frandsen E V
Department of Medical Microbiology and Immunology, Faculty of Health Sciences, University of Aarhus, Denmark.

APMIS - acta pathologica, microbiologica, et immunologica Scandinavica (DENMARK) May 1996, 104 (5) p321-38, ISSN 0903-4641 Journal Code: 8803400

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

IgA1 protease activity, which allows bacteria to cleave human IgA1 in the hinge region, represents a striking example of convergent evolution of a specific property in bacteria. Although it has been known since 1979 that IgA1 protease is produced by the three leading causes of bacterial meningitis in addition to important urogenital pathogens and some members of the oropharyngeal flora, the exact role of this enzyme in bacterial pathogenesis is still incompletely understood owing to lack of a satisfactory animal model. Cleavage of IgA1 by these post-proline **endopeptidases** efficiently separates the monomeric antigen-binding fragments from the secondary effector functions of the IgA1 antibody molecule. Several in vivo and in vitro observations indicate that the enzymes are important for the ability of bacteria to colonize mucosal membranes in the presence of S-IgA antibodies. Furthermore, the extensive cleavage of IgA sometimes observed in vivo, suggests that IgA1 protease activity results in a local functional IgA deficiency that may facilitate colonization of other microorganisms and the penetration of potential allergens. It has been hypothesized that IgA1 protease activity of *Haemophilus influenzae*, *Neisseria meningitidis*, and *Streptococcus pneumoniae*, under special immunological circumstances, allows these bacteria to take advantage of specific IgA1 antibodies in a strategy to evade other immune factors of the human body. The decisive factor is the balance between IgA antibodies against surface antigens of the respective bacteria and their IgA1 protease. Recent studies have shown that serine-type IgA1 proteases of *H. influenzae*, meningococci, and gonococci belong to a family of proteins used by a diverse group of Gram-negative bacteria for colonization and invasion. (155 Refs.)

Tags: Animal; Human

Descriptors: Bacteria--enzymology--EN; *Bacteria--pathogenicity--PY; *Bacterial Infections--enzymology--EN; *Bacterial Infections--microbiology--MI; *Immunoglobulin A--physiology--PH; * **Serine Endopeptidases** --physiology --PH; Amino Acid Sequence; Bacteria--immunology--IM; Bacterial Infections--immunology--IM; Molecular Sequence Data; Virulence

CAS Registry No.: 0 (Immunoglobulin A)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19960909

Record Date Completed: 19960909

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DIALOG(R) File 155:MEDLINE(R)

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10449888 96256608 PMID: 8655552

The cryptic general secretory pathway (gsp) operon of Escherichia coli K-12 encodes functional proteins.

Francetic O; Pugsley A P

Unite de Genetique Moleculaire, Centre National de la Recherche Scientifique Unite de Recherche Associee 1149, Institut Pasteur, Paris, France.

Journal of bacteriology (UNITED STATES) Jun 1996, 178 (12) p3544-9, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Systematic sequencing of the *Escherichia coli* K-12 chromosome (GenBank entry U18997) has revealed the presence of an apparently complete operon of genes (the *gspC-0* operon) similar to genes coding for components of the main terminal branch of the general secretory pathway (e.g., the *Klebsiella oxytoca pulC-0* pullulanase secretion operon) and to related genes required for type IV pilus biogenesis. For example, the last gene in the *gsp* operon, *gspO* (formerly *hopD*), encodes a protein which is similar to several type IV prepilin peptidases. Expression of *gspO* from *lacZp* promotes cleavage of two known prepilin peptidase substrates in *E. coli* K-12: *Neisseria gonorrhoeae* type IV prepilin and *K. oxytoca* prePulG protein. *gspO* also complements a mutation in the corresponding gene (*pulO*) of the pullulanase secretion operon when it is expressed from *lacZp*. Another gene in the *gsp* operon, *gspG* (formerly *hopG*), encodes a protein similar to prePulG, a component of the pullulanase secretion pathway. Expression of *gspG* from *lacZp* leads to production of a protein which (i) is recognized by PulG-specific antiserum (and by antiserum against the *Pseudomonas aeruginosa* PulG homolog XcpG [formerly XcpT]), (ii) is processed in cells expressing *gspO*, and (iii) restores secretion in cells carrying a *pulG* mutation. The chromosomal copies of *gspG* and *gspO* are apparently not expressed, probably because of very weak transcription from the upstream region, as measured by using a chromosomal *gspC-lacZ* operon fusion. Thus, the *gsp* operon of *E. coli* K-12 includes at least two functional genes which, together with the rest of the operon, are probably not expressed under laboratory conditions.

Tags: Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--genetics--GE; *Bacterial Proteins--secretion--SE; **Escherichia coli*--genetics--GE; Bacterial Outer Membrane Proteins--metabolism--ME; Base Sequence; DNA, Bacterial--genetics--GE; **Endopeptidases** --genetics--GE; Fimbriae Proteins; Gene Expression Regulation, Bacterial; Genes, Structural, Bacterial; Genetic Complementation Test; Glycoside Hydrolases--genetics--GE; Molecular Sequence Data; Operon; Promoter Regions (Genetics); RNA, Messenger --genetics--GE; Regulatory Sequences, Nucleic Acid; Transcription, Genetic Molecular Sequence Databank No.: GENBANK/U18997

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Bacterial Proteins); 0 (DNA, Bacterial); 0 (RNA, Messenger); 147680-16-8 (Fimbriae Proteins)

Enzyme No.: EC 3.2.1. (Glycoside Hydrolases); EC 3.2.1.41 (pullulanase); EC 3.4.- (**Endopeptidases**)

Record Date Created: 19960730

Record Date Completed: 19960730

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DIALOG(R) File 155:MEDLINE(R)

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10381215 96186495 PMID: 8641803

Analysis of the specificity of bacterial immunoglobulin A (IgA) proteases by a comparative study of ape serum IgAs as substrates.

Qiu J; Brackee G P; Plaut A G

Gastroenterology Division, Department of Medicine, Tufts-New England Medical Center, Boston, Massachusetts 02111, USA.

Infection and immunity (UNITED STATES) Mar 1996, 64 (3) p933-7, ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: NIDR-DE 06977; DE; NIDCR

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Immunoglobulin A (IgA) proteases are bacterial enzymes with substrate specificity for human serum and secretory IgAs. To further define the basis of this specificity, we examined the ability of IgA proteases of *Clostridium ramosum*, *Streptococcus pneumoniae* (EC 3.4.24.13), *Neisseria meningitidis* (EC 3.4.21.72), and *Haemophilus influenzae* (EC 3.4.21.72) to

Institute of Medical Microbiology, University of Aarhus, Denmark.
Vaccine (ENGLAND) Sep 1995, 13 (13) p1213-9, ISSN 0264-410X
Journal Code: 8406899

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The antigenic diversity among IgA1 proteases of 61 *Neisseria* gonorrhoeae strains isolated during a period of 23 years and on four continents was examined in enzyme neutralization assays employing rabbit antisera raised against selected IgA1 proteases. The antigenic analyses were compared with results of iga gene-region RFLP patterns and enzyme cleavage specificity for substrate IgA1. Type 1 IgA1 proteases were antigenically uniform while six different antigenic types were detected among type 2 enzymes. Extensive cross-reactions of antibodies against the different antigenic types suggested only minor differences in relevant epitopes. Epitopes previously found to be common to all *Neisseria* meningitidis IgA1 proteases were also shared by all *N. gonorrhoeae* IgA1 proteases in the collection. Human sera from patients with gonorrhoea showed broadly cross-reactive neutralizing activity at titers comparable to those of sera from immunized rabbits. In conclusion, *N. gonorrhoeae* IgA1 proteases show a remarkable lack of diversity of epitopes recognized by enzyme-neutralizing antibodies. If future studies confirm that cleavage of IgA1 is an important step in gonococcal infections, *Neisseria* IgA1 proteases may be attractive vaccine candidates.

Tags: Animal; Comparative Study; Human; Support, Non-U.S. Gov't
Descriptors: Cross Reactions; *Epitope Mapping; * *Neisseria* gonorrhoeae --physiology--PH; * **Serine Endopeptidases** --immunology --IM; Epitopes; Genes, Bacterial; Immunoglobulin A--genetics--GE; *Neisseria* gonorrhoeae --enzymology--EN; *Neisseria* gonorrhoeae--immunology--IM; Neutralization Tests; Polymorphism, Restriction Fragment Length; Rabbits; Serotyping; Substrate Specificity
CAS Registry No.: 0 (Epitopes); 0 (Immunoglobulin A)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)
Record Date Created: 19960308
Record Date Completed: 19960308

9/9/13
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

10222271 96023519 PMID: 7548543
Comparative studies of the IgA1 protease genes from Haemophilus influenzae, Neisseria gonorrhoeae, and Prevotella melaninogenica.

Arzese A; Botta G A
Institute of Microbiology, School of Medicine, University of Udine, Italy.

Clinical infectious diseases - an official publication of the Infectious Diseases Society of America (UNITED STATES) Jun 1995, 20 Suppl 2 pS169-71, ISSN 1058-4838 Journal Code: 9203213

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Comparative Study; Human; Support, Non-U.S. Gov't
Descriptors: Haemophilus influenzae--enzymology--EN; * *Neisseria* gonorrhoeae--enzymology--EN; *Prevotella--enzymology--EN; * **Serine Endopeptidases** --genetics --GE; Genes, Bacterial; Haemophilus influenzae --genetics--GE; Immunoglobulin A; *Neisseria* gonorrhoeae--genetics--GE; Prevotella--genetics--GE

CAS Registry No.: 0 (Immunoglobulin A)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)
Gene Symbol: iga
Record Date Created: 19951102

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DIALOG(R) File 155:MEDLINE(R)

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10219448 96020667 PMID: 7476198

SepA, the major extracellular protein of *Shigella flexneri*: autonomous secretion and involvement in tissue invasion.

Benjelloun-Touimi Z; Sansonetti P J; Parsot C

Unite de Pathogenie Microbienne Moleculaire, INSERM U389, Institut Pasteur, Paris, France.

Molecular microbiology (ENGLAND) Jul 1995, 17 (1) p123-35, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

In addition to Ipa proteins and IcsA, which are involved in entry into epithelial cells and intercellular spread, respectively, *Shigella* secretes a 110 kDa protein, designated SepA. We report the identification, cloning, and nucleotide sequence determination of the *sepA* gene, analysis of SepA secretion, and construction and characterization of a *sepA* mutant. The *sepA* gene is carried by the virulence plasmid and codes for a 150 kDa precursor. Upon secretion, which does not involve accessory proteins encoded by the virulence plasmid, the precursor is converted to a mature protein of 110 kDa by two cleavages removing an N-terminal signal sequence and a C-terminal fragment. Extensive similarities were detected between the sequence of the first 500 residues of mature SepA and the N-terminal region of IgA1 proteases from *Neisseria gonorrhoeae* and *Haemophilus influenzae*, the Tsh haemagglutinin of an avian pathogenic *Escherichia coli*, and the Hap protein involved in adhesion and penetration of *H. influenzae*. The C-terminal domain of the SepA precursor, which is not present in the secreted protein, exhibits sequence similarity with pertactin of *Bordetella pertussis* and the ring-forming protein of *Helicobacter mustelae*. Construction and phenotypic characterization of a *sepA* mutant indicated that SepA is required neither for entry into cultured epithelial cells nor for intercellular dissemination. However, in the rabbit ligated ileal loop model, the *sepA* mutant exhibited an attenuated virulence, which suggests that SepA might play a role in tissue invasion.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--physiology--PH; *Bacterial Proteins--secretion--SE; *Genes, Structural, Bacterial--genetics--GE; **Shigella flexneri*--pathogenicity--PY; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Cloning, Molecular; Ileum--microbiology--MI; Immunoglobulin A--metabolism--ME; Molecular Sequence Data; Mucous Membrane--microbiology--MI; Mutation; Plasmids--genetics--GE; Protein Precursors--genetics--GE; Protein Processing, Post-Translational; Rabbits; Sequence Analysis; Sequence Analysis, DNA; Sequence Homology, Amino Acid; **Serine Endopeptidases** --metabolism --ME; *Shigella flexneri*--genetics--GE; Virulence

Molecular Sequence Databank No.: GENBANK/Z48219

CAS Registry No.: 0 (Bacterial Proteins); 0 (Immunoglobulin A); 0 (Plasmids); 0 (Protein Precursors); 0 (SepA protein, *Shigella*)

Enzyme No.: EC 3.4.21 (**Serine Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19951218

Record Date Completed: 19951218

9/9/15

DIALOG(R) File 155:MEDLINE(R)

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10200531 96001589 PMID: 8525999

Titration of inhibiting antibodies to bacterial IgA1 proteases in human sera and secretions.

Reinholdt J; Kilian M
Royal Dental College, Faculty of Health Sciences, University of Aarhus,
Denmark.

Advances in experimental medicine and biology (UNITED STATES) 1995,
371A p605-8, ISSN 0065-2598 Journal Code: 0121103

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Tags: Human

Descriptors: Antibodies, Bacterial--analysis--AN; *Antigens, Bacterial
--immunology--IM; *Bacterial Proteins--immunology--IM; *Colostrum
--immunology--IM; *Saliva--immunology--IM; *Salivary Proteins--immunology
--IM; * **Serine Endopeptidases** --immunology --IM; Antibodies, Bacterial
--blood--BL; Antibodies, Bacterial--immunology--IM; Antibody Specificity;
Bacterial Proteins--antagonists and inhibitors--AI; Haemophilus influenzae
--immunology--IM; Immunoglobulin A, Secretory--immunology--IM;
Immunoglobulin A, Secretory--isolation and purification--IP; **Neisseria**
meningitidis--immunology--IM; Streptococcus--immunology--IM

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antigens, Bacterial);
0 (Bacterial Proteins); 0 (Immunoglobulin A, Secretory); 0 (Salivary
Proteins)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72
(IgA-specific serine endopeptidase)

Record Date Created: 19960124

Record Date Completed: 19960124

9/9/16

DIALOG(R) File 155:MEDLINE(R)

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10200530 96001588 PMID: 8525998

**Antigenic and genetic heterogeneity among Haemophilus influenzae and
Neisseria IgA1 proteases.**

Lomholt H; Poulsen K; Kilian M

Institute of Medical Microbiology, University of Aarhus, Denmark.

Advances in experimental medicine and biology (UNITED STATES) 1995,
371A p599-603, ISSN 0065-2598 Journal Code: 0121103

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

(18 Refs.)

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: Antigens, Bacterial--genetics--GE; *Bacterial Proteins
--genetics--GE; *Haemophilus influenzae--enzymology--EN; *Immunoglobulin A
--metabolism--ME; * **Neisseria** --enzymology--EN; * **Serine Endopeptidases**
--genetics --GE; Antigens, Bacterial--immunology--IM; Bacterial Proteins
--immunology--IM; Evolution, Molecular; Genes, Structural, Bacterial;
Haemophilus influenzae--genetics--GE; Haemophilus influenzae--immunology
--IM; **Neisseria** --genetics--GE; **Neisseria** --immunology--IM; Phylogeny;
Polymorphism, Restriction Fragment Length; **Serine Endopeptidases**
--immunology --IM; Species Specificity; Substrate Specificity

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Proteins); 0
(Immunoglobulin A)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72
(IgA-specific serine endopeptidase)

Record Date Created: 19960124

Record Date Completed: 19960124

9/9/17

DIALOG(R) File 155:MEDLINE(R)

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08614434 95302961 PMID: 7783620

01865495 75040397 PMID: 4214777

Studies on gonococcus infection. VI. Electron microscopic study on in vitro phagocytosis of gonococci by human leukocytes.

Swanson J ; Zeligs B

Infection and immunity (UNITED STATES) Sep 1974 , 10 (3) p645-56,
ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Tags: Human

Descriptors: Leukocytes--immunology--IM; * *Neisseria gonorrhoeae*
--immunology--IM; *Phagocytosis; Histological Techniques; Leukocytes
--ultrastructure--UL; Microscopy, Electron; Microscopy, Electron, Scanning;
Neisseria gonorrhoeae--ultrastructure--UL

Record Date Created: 19750129

Record Date Completed: 19750129

3/9/2

DIALOG(R) File 155:MEDLINE(R)

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01865494 75040396 PMID: 4214776

Studies on gonococcus infection. V. Observations on in vitro interactions of gonococci and human neutrophils.

Swanson J ; Sparks E; Zeligs B; Siam M A; Parrott C

Infection and immunity (UNITED STATES) Sep 1974 , 10 (3) p633-44,
ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Tags: Human

Descriptors: *Neisseria gonorrhoeae*--immunology--IM; *Neutrophils
--immunology--IM; Carbon Radioisotopes; Cell Adhesion--drug effects--DE;
Cell Separation; Chymotrypsin--pharmacology--PD; Glutaral--pharmacology--PD
; Heat; Hela Cells--immunology--IM; Microscopy, Electron; *Neisseria*
gonorrhoeae--cytology--CY; *Neisseria gonorrhoeae*--ultrastructure--UL;
Neutrophils--cytology--CY; Phagocytosis--drug effects--DE; Trypsin
--pharmacology--PD

CAS Registry No.: 0 (Carbon Radioisotopes); 111-30-8 (Glutaral)

Enzyme No.: EC 3.4.21.1 (Chymotrypsin); EC 3.4.21.4 (Trypsin)

Record Date Created: 19750129

Record Date Completed: 19750129

3/9/3

DIALOG(R) File 155:MEDLINE(R)

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01738316 74149824 PMID: 4207517

Differential attachment by piliated and nonpiliated *Neisseria gonorrhoeae* to human sperm.

James-Holmquest A N; Swanson J ; Buchanan T M; Wende R D; Williams R P

Infection and immunity (UNITED STATES) May 1974 , 9 (5) p897-902,
ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Tags: Animal; Human; In Vitro; Male

Descriptors: *Neisseria gonorrhoeae*--immunology--IM; *Spermatozoa
--immunology--IM; Antibody Specificity; Bacteriological Techniques; Cell
Adhesion; Cell Wall; *Escherichia coli*--immunology--IM; Formaldehyde; Heat;
Immune Sera; Immunoglobulin G; Microscopy, Electron; Rabbits--immunology

diversity of serogroup A bacteria seems quite limited and only a few strains have been responsible for the epidemics of recent decades. Meningococci express both constant and highly variable antigens, the variability of which is determined by the clonal background of the epidemic strain. The development of an improved vaccine is being pursued but still faces technical problems. (58 Refs.)

Tags: Human

Descriptors: *Meningitis, Meningococcal--epidemiology--EP; *Neisseria meningitidis--genetics--GE; Antigens, Bacterial--immunology--IM; Disease Outbreaks; Isoenzymes--analysis--AN; Neisseria meningitidis--classification--CL; Neisseria meningitidis--immunology--IM

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Isoenzymes)

Record Date Created: 19920428

Record Date Completed: 19920428

1/9/3

DIALOG(R) File 155:MEDLINE(R)

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07070187 91311103 PMID: 1906911

Variation in class 5 protein expression by serogroup A meningococci during a meningitis epidemic.

Achtman M ; Wall R A; Bopp M; Kusecek B; Morelli G; Saken E; Hassan-King M

Max-Planck-Institut fur molekulare Genetik, Berlin, Germany.

Journal of infectious diseases (UNITED STATES) Aug 1991 , 164 (2)
p375-82, ISSN 0022-1899 Journal Code: 0413675

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

Serogroup A meningococci were isolated from patients and healthy carriers in The Gambia between 1982 and 1988. The class 5 proteins expressed by these bacteria were identified by electrophoretic migration and by serologic tests. Three protein serologic groupings (seroclasses) called A (protein 5a), B (proteins 5b, 5d, or 5e), and C (protein 5c or 5C) were found among 331 bacterial isolates. The number of class 5 proteins expressed per isolate varied from none to four, with a median of two. The class 5 protein composition differed for certain paired isolates obtained from the nasopharynx, blood, and cerebrospinal fluid of diseased patients and for certain pairs of sequential isolates from the nasopharynx of healthy carriers; the medical relevance of this variation remains unclear, although the 5C protein was preferentially isolated from the nasopharynx and the 5a protein from diseased patients. The data show that a large proportion of healthy carriers in The Gambia were exposed to bacteria expressing each of the three seroclasses and that many people were exposed to bacteria expressing each of the three seroclasses and that many people were exposed to two or all three seroclasses during the epidemic of 1982-1983.

Tags: Human; Support, Non-U.S. Gov't

Descriptors: *Disease Outbreaks; *Meningitis, Meningococcal--microbiology--MI; *Neisseria meningitidis--metabolism--ME; *Viral Proteins--biosynthesis--BI; Antibodies, Monoclonal--immunology--IM; Blotting, Western; Carrier State--microbiology--MI; Conjunctiva--microbiology--MI; Gambia--epidemiology--EP; Gene Expression Regulation, Bacterial; Meningitis, Meningococcal--blood--BL; Meningitis, Meningococcal--cerebrospinal fluid--CF; Meningitis, Meningococcal--epidemiology--EP; Nasopharynx--microbiology--MI; Neisseria meningitidis--classification--CL; Neisseria meningitidis--genetics--GE; Septicemia--microbiology--MI; Serotyping; Viral Proteins--genetics--GE

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Viral Proteins)

Record Date Created: 19910823

Record Date Completed: 19910823

1/9/4

DIALOG(R) File 155:MEDLINE(R)

07398035 92261288 PMID: 1813777

Cloning and expression in Escherichia coli of opc, the gene for an unusual class 5 outer membrane protein from Neisseria meningitidis (meningococci/surface antigen).

Olyhoek A J; Sarkari J; Bopp M; Morelli G; **Achtman M**

Max-Planck Institut fur molekulare Genetik, Berlin, Germany.

Microbial pathogenesis (ENGLAND) Oct 1991, 11 (4) p249-57, ISSN 0882-4010 Journal Code: 8606191

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A genomic library was constructed in a lambda gt11 vector using chromosomal DNA from a meningococcal serogroup A strain and plaques expressing the class 5C protein were recognized by screening with specific monoclonal antibodies. The opc insert was subcloned into a multicopy plasmid which induced expression of that protein in Escherichia coli as a surface-exposed major outer membrane protein. The nucleotide sequence of opc is typical of an outer membrane protein with a promoter and terminator region, a leader peptide which is cleaved during expression and a complete open reading frame. Unlike other meningococcal class 5 proteins or gonococcal P.II proteins, the sequence did not contain any pentanucleotide repeats and the sequence showed little homology to these other functionally related proteins. However, the predicted amino acid sequence of the mature protein for opc showed 27% similarity to that for a second opa gene cloned from the same meningococcal strain. This is the first report of cloning and expression of a functional meningococcal gene encoding a class 5 outer membrane protein in E. coli.

Tags: Support, Non-U.S. Gov't

Descriptors: *Bacterial Outer Membrane Proteins--genetics--GE; *Escherichia coli--genetics--GE; *Neisseria meningitidis--genetics--GE; Amino Acid Sequence; Antibodies, Monoclonal; Antigens, Bacterial--chemistry--CH; Antigens, Bacterial--genetics--GE; Antigens, Surface--chemistry--CH; Antigens, Surface--genetics--GE; Base Sequence; Blotting, Southern; Blotting, Western; Cloning, Molecular; DNA, Bacterial--genetics--GE; Electrophoresis, Polyacrylamide Gel; Gene Expression; Genes, Bacterial; Molecular Sequence Data; Neisseria meningitidis--chemistry--CH; Neisseria meningitidis--immunology--IM; Repetitive Sequences, Nucleic Acid; Translation, Genetic

Molecular Sequence Databank No.: GENBANK/M80195; GENBANK/S72518; GENBANK/S72520; GENBANK/S78944; GENBANK/S78945; GENBANK/S78946; GENBANK/S78947; GENBANK/S78948; GENBANK/S78949; GENBANK/S78950

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Antigens, Bacterial); 0 (Antigens, Surface); 0 (Bacterial Outer Membrane Proteins); 0 (DNA, Bacterial); 147335-96-4 (opc protein).

Record Date Created: 19920616

Record Date Completed: 19920616

1/9/2

DIALOG(R) File 155:MEDLINE(R)

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07342709 92205828 PMID: 1803694

Clonal properties of meningococci from epidemic meningitis.

Achtman M

Max-Planck Institut fur Molekulare Genetik, Berlin, Germany.

Transactions of the Royal Society of Tropical Medicine and Hygiene (ENGLAND) 1991, 85 Suppl 1 p24-31, ISSN 0035-9203 Journal Code: 7506129

Document type: Journal Article; Review; Review, Academic

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Methods from the field of population genetics now enable the classification of epidemic strains of Neisseria meningitidis and have resolved the relationships between apparently distinct epidemics. The

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07069402 91310318 PMID: 1677349

Virulence patterns and long-range genetic mapping of extraintestinal Escherichia coli K1, K5, and K100 isolates: use of pulsed-field gel electrophoresis.

Ott M; Bender L; Blum G; Schmittroth M; **Achtman M** ; Tschape H; Hacker J
Institut fur Genetik und Mikrobiologie, Universitat Wurzburg, Germany.

Infection and immunity (UNITED STATES) Aug 1991 , 59 (8) p2664-72,
ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A total of 127 extraintestinal Escherichia coli strains of the capsule serotypes K1, K5, and K100 from human and animal sources were analyzed for DNA sequences specific for the genes for various adhesins (P fimbriae [pap] and P-related sequences [prs], S fimbriae [sfa]/F1C fimbriae [foc], and type I fimbriae [fim]), aerobactin (aer), and hemolysin (hly). The expression of corresponding virulence factors was also tested. Twenty-four selected strains were analyzed by long-range DNA mapping to evaluate their genetic relationships. DNA sequences for the adhesins were often found in strains not expressing them, while strains with hemolysin and aerobactin genes usually did express them. Different isolates of the same serotype often expressed different virulence patterns. The use of virulence-associated gene probes for Southern hybridization with genomic DNA fragments separated by pulsed-field gel electrophoresis revealed that a highly heterogeneous restriction fragment length and hybridization pattern existed even within strains of the same serotype. Long-range DNA mapping is therefore useful for the evaluation of genetic relatedness among individual isolates and facilitates the performance of precise molecular epidemiology.

Tags: Animal; Human; Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--genetics--GE; *Escherichia coli --genetics--GE; *Genes, Bacterial; Adhesins, Escherichia coli; Bacterial Outer Membrane Proteins--genetics--GE; Blotting, Southern; Chromosome Mapping; DNA Probes; Electrophoresis, Agar Gel; Escherichia coli --classification--CL; Escherichia coli--isolation and purification--IP; Escherichia coli--pathogenicity--PY; Fimbriae, Bacterial; Hemolysins --genetics--GE; Hydroxamic Acids--metabolism--ME; Phenotype; Polymorphism, Restriction Fragment Length; Serotyping; Virulence--genetics--GE

CAS Registry No.: 0 (Adhesins, Escherichia coli); 0 (Bacterial Outer Membrane Proteins); 0 (Bacterial Proteins); 0 (DNA Probes); 0 (Hemolysins); 0 (Hydroxamic Acids); 26198-65-2 (aerobactin)

Record Date Created: 19910823

Record Date Completed: 19910823

1/9/5

DIALOG(R)File 155:MEDLINE(R)

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06928036 91168426 PMID: 1706236

Human hybridomas derived from CD5+ B lymphocytes of patients with chronic lymphocytic leukemia (B-CLL) produce multi-specific natural IgM (kappa) antibodies.

Jahn S; Schwab J; Hansen A; Heider H; Schroeder C; Lukowsky A; **Achtman M** ; Matthes H; Kiessig S T; Volk H D; et al

Department of Medical Immunology, Medical School (Charite), Humboldt University, Berlin, Germany.

Clinical and experimental immunology (ENGLAND) Mar 1991 , 83 (3) p413-7, ISSN 0009-9104 Journal Code: 0057202

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Great numbers of CD5+ B lymphocytes were detected in the peripheral blood of patients with B-CLL. To study the antibody repertoire of this immune

cell subpopulation on a monoclonal level, we fused the lymphocytes derived from five different donors to a highly efficient HAT-sensitive heteromyeloma line (CB-F7). A fusion frequency of up to 10^{-5} allowed us to analyse hundreds of initial hybridoma lines per fusion. In all culture supernatants in three out of five fusions IgM lambda antibodies were detected, in two experiments only IgM kappa was measured, suggesting monoclonality of the primary hybridoma cell lines. The later fusions resulted in hybridomas producing multi-specific antibodies against both an autoantigen and an infectious agent: (i) dsDNA/influenza virus haemagglutinin; (ii) dsDNA/class V outer membrane protein type C from *Neisseria meningitidis*. However, no antibodies of the described specificity were detected in blood sera of patients, indicating a 'switch-on' of the immunoglobulin secretion capacity of malignant B cells during fusion to a myeloma partner. We discuss the results as further evidence for the natural multi-reactive antibody repertoire of CD5+ B cells.

Tags: Female; Human; Male

Descriptors: *Antigens, CD--physiology--PH; *Antigens, Differentiation--physiology--PH; *B-Lymphocytes--immunology--IM; *Immunoglobulin M--biosynthesis--BI; *Leukemia, B-Cell, Chronic--immunology--IM; Adult; Aged; Antibodies, Monoclonal--biosynthesis--BI; Antibody Specificity; Antigens, CD5; Hybridomas--metabolism--ME; Immunoglobulins, kappa-Chain--biosynthesis--BI; Middle Age; Tumor Cells, Cultured

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Antigens, CD); 0 (Antigens, CD5); 0 (Antigens, Differentiation); 0 (Immunoglobulin M); 0 (Immunoglobulins, kappa-Chain)

Record Date Created: 19910419

Record Date Completed: 19910419

--IM

CAS Registry No.: 0 (Immune Sera); 0 (Immunoglobulin G); 50-00-0
(Formaldehyde)

Record Date Created: 19740625

Record Date Completed: 19740625

3/9/4

DIALOG(R) File 155:MEDLINE(R)

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01710172 74118041 PMID: 4205885

Gonococcal ophthalmia neonatorum. Relationship of time of infection to relevant control measures.

Thompson T R; Swanson R E ; Wiesner P J

JAMA - the journal of the American Medical Association (UNITED STATES)

Apr 8 1974 , 228 (2) p186-8, ISSN 0098-7484 Journal Code: 7501160

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

Tags: Female; Human; Pregnancy

Descriptors: *Ophthalmia Neonatorum--etiology--ET; Adolescent; Adult;
Conjunctivitis--diagnosis--DI; Eye--microbiology--MI; Fetal Diseases
--diagnosis--DI; Gonorrhea--complications--CO; Infant, Newborn;
Maternal-Fetal Exchange; **Neisseria** gonorrhoeae --isolation and
purification--IP; Ophthalmia Neonatorum--drug therapy--DT; Ophthalmia
Neonatorum--prevention and control--PC; Pregnancy Complications, Infectious
; Prenatal Diagnosis; Silver Nitrate--therapeutic use--TU

CAS Registry No.: 7761-88-8 (Silver Nitrate)

Record Date Created: 19740507

Record Date Completed: 19740507

10605582 96423170 PMID: 8825771

A physical and genetic map of *Neisseria meningitidis* B1940.

Gaher M; Einsiedler K; Crass T; Bautsch W

Institut für Medizinische Mikrobiologie, Medizinische Hochschule
Hannover, Germany.

Molecular microbiology (ENGLAND) Jan 1996, 19 (2) p249-59, ISSN
0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A physical map of the chromosome of *Neisseria meningitidis* B1940 has been constructed by one- and two-dimensional pulsed-field gel electrophoresis techniques. Complete macrorestriction maps for the enzymes *NheI* (16 sites), *SgfI* (13 sites), *SfiI* (11 sites) and *I-CeuI* (4 sites), as well as a partial restriction map for the restriction enzyme *SpeI* (15 of c. 28 sites) could be established. Altogether, 59 restriction sites were mapped on a single circular chromosome of 2.3 Mbp. By restriction endonuclease digestion and Southern hybridization of cloned genetic markers, 39 genetic loci were assigned to this map. Comparison with the metabolic maps of *Neisseria gonorrhoeae* MS11-N198 and FA1090 revealed a high degree of conservation in the arrangement of gene loci among these two species, although four out of 24 genetic loci are located at different chromosomal positions, indicating several genomic rearrangements.

Tags: Support, Non-U.S. Gov't

Descriptors: Chromosome Mapping; *Chromosomes, Bacterial--genetics--GE;
*Genome, Bacterial; * *Neisseria meningitidis* --genetics--GE; DNA
Restriction Enzymes--metabolism--ME; *Neisseria meningitidis* --isolation
and purification--IP; Restriction Mapping

Enzyme No.: EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19961205

Record Date Completed: 19961205

8/9/2

DIALOG(R) File 155:MEDLINE(R)

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10260590 96062220 PMID: 7592413

The physical map of the chromosome of a serogroup A strain of *Neisseria meningitidis* shows complex rearrangements relative to the chromosomes of the two mapped strains of the closely related species *N. gonorrhoeae*.

Dempsey J A; Wallace A B; Cannon J G

Department of Microbiology and Immunology, University of North Carolina
School of Medicine, Chapel Hill 27599, USA.

Journal of bacteriology (UNITED STATES) Nov 1995, 177 (22) p6390-400
, ISSN 0021-9193 Journal Code: 2985120R

Contract/Grant No.: AI23830; AI; NIAID; AI28807; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A physical map of the chromosome of *N. meningitidis* Z2491 (serogroup A, subgroup IV-1) has been constructed. Z2491 DNA was digested with *NheI*, *SpeI*, *SgfI*, *PacI*, *BglII*, or *PmeI*, resulting in a limited number of fragments that were resolved by contour-clamped homogeneous electric field (CHEF) electrophoresis. The estimated genome size for this strain was 2,226 kb. To construct the map, probes corresponding to single-copy genes or sequences were used on Southern blots of chromosomal DNA digested with the different mapping enzymes and subjected to CHEF electrophoresis. By determining which fragments from different digests hybridized to each specific probe, it was possible to walk back and forth between digests to form a circular macrorestriction map. The intervals between mapped restriction sites range from 10 to 143 kb in size. A total of 117 markers have been placed on the map; 75 represent identified genes, with the remaining markers defined by anonymous cloned fragments of *neisserial* DNA. Comparison of the arrangement of genetic loci in Z2491 with that in

gonococcal strain FA1090, for which a physical map was previously constructed, revealed complex genomic rearrangements between the two strains. Although gene order is generally conserved over much of the chromosome, a region of approximately 500 kb shows translocation and/or inversion of multiple blocks of markers between the two strains. Even within the relatively conserved portions of the maps, several genetic markers are in different positions in Z2491 and FA1090.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: Chromosomes, Bacterial; *Gene Rearrangement; * **Neisseria gonorrhoeae**--genetics--GE; * **Neisseria meningitidis** --genetics--GE; *Restriction Mapping; Base Sequence; Chromosome Walking--methods--MT; DNA Probes; Deoxyribonucleases, Type II Site-Specific; Electrophoresis, Gel, Pulsed-Field; Genetic Markers; Inversion (Genetics); Molecular Sequence Data; Translocation (Genetics)

CAS Registry No.: 0 (DNA Probes); 0 (Genetic Markers)

Enzyme No.: EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific)

Record Date Created: 19951219

Record Date Completed: 19951219

?logoff hold

YSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2003/Oct W4

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*File 155: Please see HELP NEWS 155 for details about the 2003 reload.

File 654:US Pat.Full. 1976-2003/Oct 30

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*File 654: US published applications now online. See HELP NEWS 654 for details. Reassignments current through August 4, 2003.

File 5:Biosis Previews(R) 1969-2003/Oct W4

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*File 5: BIOSIS Previews has been reloaded with major enhancements.

See HELP NEWS005 for more information.

File 73:EMBASE 1974-2003/Oct W4

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File 348:EUROPEAN PATENTS 1978-2003/Oct W04

(c) 2003 European Patent Office

File 203:AGRIS 1974-2003/Sep

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File 94:JICST-Eplus 1985-2003/Nov W1

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File 444:New England Journal of Med. 1985-2003/Nov W1

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File 156:ToxFile 1965-2003/Oct W4

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*File 156: Please see HELP NEWS 156 for information regarding the 2003 reload.

File 357:Derwent Biotech Res. _1982-2003/Nov W2

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File 35:Dissertation Abs Online 1861-2003/Sep

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File 340:CLAIMS(R)/US Patent 1950-03/Oct 30

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Set Items Description

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Cost is in DialUnits

?ds

Set	Items	Description
S1	486	MENINGI? (50N) GONO? (50N) LACTAMIC?
S2	343	RD (unique items)
S3	202	S2 AND (DNA? OR NUCLEIC? OR NUCLEOTID? OR NUCLEIC?)
S4	208	S2 AND (PROBE? OR PRIMER? OR OLIGONUCLEI? OR CDNA? OR POLY-NUCLEOT? OR NUCLEOTID? OR NUCLEIC? OR NUCLEAR? OR DNA OR ANTI-SENSE?)
S5	111	S4/1996:2003
S6	97	S4 NOT S5

?t s6/9/1-23 54

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2003/Oct W4

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*File 155: Please see HELP NEWS 155 for details about the 2003 reload.

File 654:US Pat.Full. 1976-2003/Oct 30

(c) Format only 2003 The Dialog Corp.

*File 654: US published applications now online. See HELP NEWS 654 for details. Reassignments current through August 4, 2003.

File 5:Biosis Previews(R) 1969-2003/Oct W4

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*File 5: BIOSIS Previews has been reloaded with major enhancements.

See HELP NEWS005 for more information.

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File 348:EUROPEAN PATENTS 1978-2003/Oct W04

(c) 2003 European Patent Office

File 203:AGRIS 1974-2003/Sep

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File 94:JICST-EPlus 1985-2003/Nov W1

(c)2003 Japan Science and Tech Corp(JST)

File 444:New England Journal of Med. 1985-2003/Nov W1

(c) 2003 Mass. Med. Soc.

File 156:ToxFile 1965-2003/Oct W4

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*File 156: Please see HELP NEWS 156 for information regarding the 2003 reload.

File 357:Derwent Biotech Res. _1982-2003/Nov W2

(c) 2003 Thomson Derwent & ISI

*File 357: File is now current. See HELP NEWS 357.

Alert feature enhanced for multiple files, etc. See HELP ALERT.

File 35:Dissertation Abs Online 1861-2003/Sep

(c) 2003 ProQuest Info&Learning

File 340:CLAIMS(R)/US Patent 1950-03/Oct 30

(c) 2003 IFI/CLAIMS(R)

*File 340: Enter HELP NEWS340 & HELP ALERTS340 for search, display & Alert information.

Set Items Description

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Cost is in DialUnits

?ds

Set Items Description

S1 486 MENINGI? (50N) GONO? (50N) LACTAMIC?

S2 343 RD (unique items)

S3 202 S2 AND (DNA? OR NUCLEIC? OR NUCLEOTID? OR NUCLEIC?)

S4 208 S2 AND (PROBE? OR PRIMER? OR OLIGONUCLEI? OR CDNA? OR POLY-NUCLEOT? OR NUCLEOTID? OR NUCLEIC? OR NUCLEAR? OR DNA OR ANTI-SENSE?)

S5 111 S4/1996:2003

S6 97 S4 NOT S5

?t s6/9/1-23 54

6/9/1 (Item 1 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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08492486 95180702 PMID: 7875573

Identification and characterization of specific sequences encoding pathogenicity associated proteins in the genome of commensal Neisseria species.

Wolff K; Stern A

Department of Biotechnology, TB-Z, Boehringer Mannheim GmbH, Penzberg, Germany.

FEMS microbiology letters (NETHERLANDS) Jan 15 1995, 125 (2-3)

p255-63, ISSN 0378-1097 Journal Code: 7705721

Document type: Journal Article

Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The distribution of distinct sequences in pathogenic and commensal *Neisseria* species was investigated systematically by dot blot analysis.

Probes representing the genes of *Rmp*, pilin and IgA1 protease were found to hybridize exclusively to the chromosomal DNA of the pathogenic species, *Neisseria gonorrhoeae* and/or *Neisseria meningitidis*. In contrast, specific sequences for the genes of the porin protein Por and the opacity protein (Opa) were also detected in a panel of commensal *Neisseria* species such as *N. lactamica*, *N. subflava*, *N. flava*, *N. mucosa* and *N. sicca*. Using opa-specific oligonucleotides as **probes** in chromosomal blots, the genomes of the commensal *Neisseria* species show a totally reduced repertoire of cross-hybridizing loci compared to the complex opa gene family of *N. gonorrhoeae*. DNA sequence analysis of one opa-related gene derived from *N. flava* and *N. sicca*, respectively, revealed a large degree of homology with previously described gonococcal and meningococcal genes, e.g., a typical repetitive sequence in the leader peptide and the distribution of the hypervariable and conserved regions. This observation, together with the finding, that the gene is constitutively transcribed, leads to the assumption that some of the commensal *Neisseria* species may have the potential for the expression of a protein harboring similar functions as the Opa proteins in pathogenic *Neisseriae*.

Tags: Comparative Study

Descriptors: *Antigens, Bacterial--genetics--GE; *Bacterial Outer Membrane Proteins--genetics--GE; *Genome, Bacterial; *Neisseria--genetics--GE; *Neisseria--pathogenicity--PY; Amino Acid Sequence; Base Sequence; Chromosomes, Bacterial; DNA Primers; DNA, Bacterial--genetics--GE; Fimbriae Proteins; Molecular Sequence Data; *Neisseria gonorrhoeae*--genetics--GE; *Neisseria gonorrhoeae*--pathogenicity--PY; *Neisseria meningitidis*--genetics--GE; *Neisseria meningitidis*--pathogenicity--PY; Oligonucleotide **Probes**; Sequence Homology, Amino Acid; Serine Endopeptidases--genetics--GE; Species Specificity; Virulence--genetics--GE

Molecular Sequence Databank No.: GENBANK/U12287; GENBANK/U12288

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Outer Membrane Proteins); 0 (DNA Primers); 0 (DNA, Bacterial); 0 (Oligonucleotide Probes); 0 (gonococcal protein III); 0 (opacity protein (*Neisseria gonorrhoeae*)); 147680-16-8 (Fimbriae Proteins)

Enzyme No.: EC 3.4.21 (Serine Endopeptidases); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19950404

Record Date Completed: 19950404

6/9/2 (Item 2 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

08371117 95059090 PMID: 7969193

Detection of the tetM determinant in *Neisseria gonorrhoeae* using a non-radioactively labelled oligonucleotide probe.

Carballo M; Ng L K; Dillon J R

National Laboratory for Sexually Transmitted Diseases, Laboratory Centre for Disease Control, Ottawa, Ontario, Canada.

Molecular and cellular probes (ENGLAND) Jun 1994, 8 (3) p205-8,

ISSN 0890-8508 Journal Code: 8709751

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Three oligonucleotide **probes**, complementary to tetM sequences, were labelled non-radiometrically using the DIG-oligonucleotide tailing kit and evaluated for their specificity for the detection of plasmid mediated tetracycline resistance in *Neisseria gonorrhoeae*. Only **Probe 3**, 5'-GCT CAA CAA TTC TGT TCC AGC-3', was specific for tetM. It hybridized with the tetM-containing 25.2-MDa plasmids from all of the 232 TRNG and the 130 PP/TRNG isolates used in the study. Its sensitivity, determined by dot-blot

hybridization, was 0.1 pg of pJ13 plasmid DNA or 10(4) cells. It did not hybridize with the DNA from non-PPNG, CMRNG and tetracycline susceptible isolates from seven other *Neisseria* species (*N. meningitidis*, *N. subflava*, *N. cinerea*, *N. lactamica*, *N. sicca*, *N. mucosa*, and *N. flavescens*), *Moraxella* spp. and *Haemophilus influenzae*. Probe 3 also hybridized to DNA of three tetracycline resistant *P. magnus* (MIC = 16 micrograms ml⁻¹) isolates which presumptively carried the tetM determinant. Therefore, probe 3 can be used by reference laboratories as a confirmatory test for TRNG, as well as isolates from other genera containing the tetM determinant.

Tags: Support, Non-U.S. Gov't

Descriptors: DNA, Bacterial--genetics--GE; **Neisseria gonorrhoeae* --genetics--GE; *Oligonucleotide Probes; *Polymerase Chain Reaction --methods--MT; Base Sequence; Molecular Sequence Data; Tetracycline Resistance--genetics--GE

CAS Registry No.: 0 (DNA, Bacterial); 0 (Oligonucleotide Probes)

Record Date Created: 19941222

Record Date Completed: 19941222

6/9/3 (Item 3 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

08134698 94200567 PMID: 8150256

Genetic diversity of the iron-binding protein (Fbp) gene of the pathogenic and commensal *Neisseria*.

Genco C A; Berish S A; Chen C Y; Morse S; Trees D L

Department of Microbiology and Immunology, Morehouse School of Medicine, Atlanta, Georgia 30310.

FEMS microbiology letters (NETHERLANDS) Feb 15 1994, 116 (2) p123-9, ISSN 0378-1097 Journal Code: 7705721

Contract/Grant No.: AI30797; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The pathogenic *Neisseria* and most commensal *Neisseria* species produce an iron-binding protein (Fbp) when grown under iron-limited conditions. In the current study, we confirmed the presence of Fbp, as well as DNA sequences homologous to the gonococcal fbp, in strains of *N. gonorrhoeae*, *N. meningitidis*, *N. cinerea*, *N. lactamica*, *N. subflava*, *N. kochii* and *N. polysaccharea*. The fbp genes from these strains were amplified by the polymerase chain reaction, digested with *StuI* or *RsaI*, and the restriction patterns examined. The patterns for the gonococcal and meningococcal fbp were virtually identical; however, variations were observed in the fbp sequences of the commensal *Neisseria* species. *N. flavescens*, *N. mucosa*, *N. sicca*, *N. ovis* and *Branhamella catarrhalis*, did not produce Fbp as detected by sodium dodecyl sulfate-polyacrylamide gel electrophoresis and reactivity with an Fbp specific monoclonal antibody, nor did they hybridize to an fbp-specific DNA probe.

Tags: Comparative Study; Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Proteins--genetics--GE; *Genes, Bacterial --genetics--GE; **Neisseria*--genetics--GE; *Variation (Genetics)--genetics--GE; Amino Acid Sequence; Antibodies, Bacterial; Antibodies, Monoclonal; Bacterial Proteins--chemistry--CH; Bacterial Proteins--immunology--IM; Base Sequence; Blotting, Southern; DNA Probes; DNA, Bacterial --analysis--AN; Molecular Sequence Data; *Neisseria gonorrhoeae*--genetics--GE; *Neisseria meningitidis*--genetics--GE; Polymerase Chain Reaction; Restriction Mapping; Sequence Analysis; Species Specificity

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antibodies, Monoclonal); 0 (Bacterial Proteins); 0 (DNA Probes); 0 (DNA, Bacterial); 0 (iron-regulated protein, bacterial)

Gene Symbol: fbp

Record Date Created: 19940509

Record Date Completed: 19940509

6/9/4 (Item 4 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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07829627 93285176 PMID: 7685283

Comparison of monoclonal antibody methods and a ribosomal ribonucleic acid probe test for Neisseria gonorrhoeae culture confirmation.

Janda W M; Wilcoski L M; Mandel K L; Ruther P; Stevens J M

Department of Pathology, University of Illinois, Chicago 60612.

European journal of clinical microbiology & infectious diseases - official publication of the European Society of Clinical Microbiology (GERMANY) Mar 1993, 12 (3) p177-84, ISSN 0934-9723 Journal Code: 8804297

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Recently, a chemiluminescent nucleic acid probe test that specifically detects the ribosomal ribonucleic acid of *Neisseria gonorrhoeae* has been released for clinical laboratory use (AccuProbe *Neisseria gonorrhoeae*). In this study, three coagglutination tests (GonoGen I, Meritec GC, and GC Omni), the GonoGen II immunofiltration method and the Micro Trak *Neisseria gonorrhoeae* fluorescent monoclonal antibody test were compared with AccuProbe for identification of gonococci. Strains tested (n = 376) included 194 *Neisseria gonorrhoeae*, 82 *Neisseria meningitidis*, 32 *Neisseria lactamica*, 32 *Neisseria* species, 32 *Moraxella catarrhalis*, 2 *Moraxella* spp. and 2 *Kingella denitrificans*. The GonoGen I, Meritec GC and GC Omni coagglutination tests produced clearly positive results for 93.8%, 92.3% and 95.9% of the gonococci, respectively. The GonoGen II unequivocally identified 91.8% and the MicroTrak fluorescent antibody test identified 90.7% with 2+ or greater fluorescence. AccuProbe identified 100% of the gonococci tested. GonoGen I and GonoGen II were 98% specific, Meritec GC was 99% specific and the specificity of the GC Omni, MicroTrak fluorescent antibody and AccuProbe tests was 100%. While antibody-based tests were reliable when results were clearly interpretable, the AccuProbe was the only confirmatory test that was 100% accurate. Serotyping studies indicate that an array of beta-lactamase positive and negative gonococcal serotypes fail to react with the monoclonal antibody-based tests in general and with the fluorescent antibody test in particular.

Tags: Comparative Study; Human

Descriptors: Antibodies, Monoclonal--immunology--IM; **Neisseria gonorrhoeae*--isolation and purification--IP; *RNA Probes; *RNA, Bacterial--genetics--GE; *RNA, Ribosomal--genetics--GE; Fluorescent Antibody Technique; Hemagglutination Tests; *Neisseria gonorrhoeae*--genetics--GE; *Neisseria gonorrhoeae*--immunology--IM

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (RNA Probes); 0 (RNA, Bacterial); 0 (RNA, Ribosomal)

Record Date Created: 19930713

Record Date Completed: 19930713

6/9/5 (Item 5 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

07629605 93084797 PMID: 1452689

Preliminary evaluation of the ligase chain reaction for specific detection of Neisseria gonorrhoeae.

Birkenmeyer L; Armstrong A S

Abbott Laboratories, North Chicago, Illinois 60064.

Journal of clinical microbiology (UNITED STATES) Dec 1992, 30 (12) p3089-94, ISSN 0095-1137 Journal Code: 7505564

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Rapid identification of *Neisseria gonorrhoeae* in clinical specimens is essential for effective control. Traditional culture requires a minimum of 24 h, and for some specimens harboring **gonococci**, the **gonococci** fail to grow or are misidentified. The recently described ligase chain reaction (LCR) is a highly specific and sensitive **DNA** amplification technique which was evaluated as an alternative to routine culture. Three LCR **probe** sets were used. Two of the **probe** sets were directed against the multi-copy *Opa* genes (*Omp-II*), while the third set was targeted against the multicopy *Pilin* genes. Each LCR **probe** set was evaluated with 260 microorganisms including 136 global isolates of *N. gonorrhoeae*, 41 isolates of *N. meningitidis*, and 10 isolates of *N. lactamica*; 26 nonpathogenic *Neisseria* strains; and 47 isolates of non-*Neisseria* species that may reside in clinical specimens. Amplification products were detected by using the IMx LCR format (Abbott Laboratories, Abbott Park, Ill.). Strains of *N. gonorrhoeae* were assayed at 270 cells per LCR (approximately 6.7×10^4 CFU/ml) with the *Opa* and *Pilin* **probes**, producing signals at least 21 and 15 times above background, respectively. In contrast, only background values were observed when testing the **probe** sets with 124 nongonococcal strains at 1.3×10^6 cells per LCR (approximately 3.2×10^8 CFU/ml). One hundred urogenital specimens were assayed by LCR, and compared with culture, the three **probes** were 100% sensitive (8 of 8) and 97.8% specific (90 of 92), resulting in an agreement of 98% (98 of 100). (ABSTRACT TRUNCATED AT 250 WORDS)

Tags: Human

Descriptors: **DNA** Ligases; **Neisseria gonorrhoeae*--genetics--GE; **Neisseria gonorrhoeae*--isolation and purification--IP; *Polymerase Chain Reaction--methods--MT; Base Sequence; **DNA** **Probes**; **DNA**, Bacterial--genetics--GE; **DNA**, Bacterial--isolation and purification--IP; Evaluation Studies; Gene Amplification; Gonorrhea--diagnosis--DI; Molecular Sequence Data; Polymerase Chain Reaction--statistics and numerical data--SN; Sensitivity and Specificity

CAS Registry No.: 0 (DNA Probes); 0 (DNA, Bacterial)

Enzyme No.: EC 6.5.1.- (DNA Ligases)

Record Date Created: 19930107

Record Date Completed: 19930107

6/9/6 (Item 6 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07596168 93051225 PMID: 1330818

Sequence analysis and relationships between meningococcal class 3 serotype proteins and other porins from pathogenic and non-pathogenic *Neisseria* species.

Ward M J; Lambden P R; Heckels J E

Department of Microbiology, Southampton University Medical School, Southampton General Hospital, UK.

FEMS microbiology letters (NETHERLANDS) Jul 15 1992, 73 (3) p283-9, ISSN 0378-1097 Journal Code: 7705721

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The presence of highly conserved regions within previously determined porin gene sequences from *Neisseria meningitidis* and *Neisseria gonorrhoeae* permitted the construction of oligonucleotide **primers** for PCR amplification of other *neisserial* porin genes. Although two separate porin genes (*porA* and *porB*) are present in *N. meningitidis* only a single fragment, corresponding to *porB*, could be amplified from this species. The amplified *porB* genes from four different meningococcal serotypes, which express the class 3 outer membrane protein, were sequenced. Amplified fragments corresponding to porin genes from *N. lactamica* and *N. sicca* were also sequenced. In common with the known *neisserial* porins, models of the organisation of the predicted proteins indicated trans-membrane structures with eight surface exposed loops. In the meningococcal class 3 proteins the main regions of sequence variation, which must be responsible for serotype specificity, were located on loops 5 and 7. A phylogenetic

analysis of the family of porins from the *Neisseria* confirmed the close relationship of the meningococcal class 3 protein with the **gonococcal** PIA protein, while the **gonococcal** PIB protein was shown to be closely related to the *N. lactamica* porin. The close relationship seen between porins of the pathogenic and non-pathogenic *Neisseriae* identified no obvious virulence-associated regions in the proteins, but did suggest that the current nomenclature for *neisseria* porin genes may need reviewing.

Tags: Support, Non-U.S. Gov't

Descriptors: *Bacterial Outer Membrane Proteins--metabolism--ME; **Neisseria*--genetics--GE; Alleles; Amino Acid Sequence; Base Sequence; Molecular Sequence Data; *Neisseria*--immunology--IM; Polymerase Chain Reaction; Porins

Molecular Sequence Databank No.: GENBANK/X65461; GENBANK/X65530; GENBANK/X65531; GENBANK/X65532; GENBANK/X65533; GENBANK/X65534

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Porins)

Gene Symbol: por; porA; porB

Record Date Created: 19921218

Record Date Completed: 19921218

6/9/7 (Item 7 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07560763 93015687 PMID: 1400191

Transformational exchanges in the dihydropteroate synthase gene of *Neisseria meningitidis*: a novel mechanism for acquisition of sulfonamide resistance.

Radstrom P; Fermer C; Kristiansen B E; Jenkins A; Skold O; Swedberg G

Chemical Center, Lund University, Sweden.

Journal of bacteriology (UNITED STATES) Oct 1992, 174 (20) p6386-93, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The **nucleotide** sequences of the chromosomal dihydropteroate synthase (dhps) genes in sulfonamide-susceptible and sulfonamide-resistant strains of *Neisseria meningitidis* of serogroups A, B and C were determined. The molecular weights and the amino acid sequences showed similarity to those of all other known dihydropteroate synthase polypeptides. Sequence comparison of the *N. meningitidis* dhps genes indicated horizontal transfer of **DNA** segments rather than point mutations as the cause for resistance in meningococci. The dhps genes in three of four sulfonamide-resistant meningococci contained identical central regions of 424 bp. Compared with the corresponding genes in susceptible strains, each central region included an insert of 6 bp. In one of the sulfonamide-resistant strains, the dhps gene was similar to the corresponding genes in the sensitive strains in its NH₂-terminal and C-terminal parts. Its central region, however, was identical to the corresponding regions of two of the other resistant genes, and thus it could be seen as a hybrid dhps gene. Transformation experiments and mapping of transformed dhps genes indicated the existence of a novel mechanism for the dissemination of sulfonamide resistance in *N. meningitidis*. The origin of the resistance-mediating segment of the gene is unknown, but hybridization results showed the presence of homologous dhps genes in *Neisseria gonorrhoeae* and *N. lactamica* but not in *N. subflava* or *Branhamella catarrhalis*.

Tags: Support, Non-U.S. Gov't

Descriptors: *Dihydropteroate Synthase--genetics--GE; **Neisseria meningitidis*--drug effects--DE; *Sulfonamides--pharmacology--PD; *Transformation, Bacterial--genetics--GE; Amino Acid Sequence; Base Sequence; Drug Resistance, Microbial--genetics--GE; Genes, Bacterial--genetics--GE; Molecular Sequence Data; *Neisseria meningitidis*--enzymology--EN; *Neisseria meningitidis*--genetics--GE; Polymerase Chain Reaction; Restriction Mapping

Molecular Sequence Databank No.: GENBANK/X68062; GENBANK/X68063; GENBANK/X68064; GENBANK/X68065; GENBANK/X68066; GENBANK/X68067; GENBANK/X68068; GENBANK/X68069

CAS Registry No.: 0 (Sulfonamides)

Enzyme No.: EC 2.5.1.15 (Dihydropteroate Synthase)

Gene Symbol: dhps

Record Date Created: 19921113

Record Date Completed: 19921113

6/9/8 (Item 8 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

07344960 92208117 PMID: 1554823

Epidemiology and molecular basis of penicillin-resistant *Neisseria meningitidis* in Spain: a 5-year history (1985-1989).

Saez-Nieto J A; Lujan R; Berron S; Campos J; Vinas M; Fuste C; Vazquez J A; Zhang Q Y; Bowler L D; Martinez-Suarez J V; et al

Laboratorio de Referencia de Meningococos, Centro Nacional de Microbiologia, Madrid, Spain.

Clinical infectious diseases - an official publication of the Infectious Diseases Society of America (UNITED STATES) Feb 1992, 14 (2) p394-402, ISSN 1058-4838 Journal Code: 9203213

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Penicillin-resistant (penr) clinical isolates of *Neisseria meningitidis*, which do not produce beta-lactamase, were first identified in Spain in 1985; the frequency of their recovery, which has been increasing in the past few years, reached 20% in 1989. Serogrouping, determination of serotypes and subtypes, and multilocus enzyme electrophoresis of the penr strains showed an extensive diversity. Resistance is due, at least in part, to a decreased affinity of penicillin-binding protein (PBP) 2 for penicillin. Similar low-affinity forms of PBP 2 are also found in penr isolates of *Neisseria lactamica*, *Neisseria polysaccharea*, and *Neisseria gonorrhoeae*. Genetic transformation of an *N. meningitidis* type strain to low-level penicillin resistance with DNA from resistant meningococci and other *Neisseria* species resulted in transformants that possessed low-affinity forms of PBP 2. These altered forms of PBP 2 have been shown to arise from recombinational events that replace parts of the PBP 2 gene with the corresponding regions from the PBP 2 genes of commensal *Neisseria* species. (34 Refs.)

Tags: Human; Support, Non-U.S. Gov't

Descriptors: *Meningitis, Meningococcal--epidemiology--EP; *Meningococcal Infections--epidemiology--EP; **Neisseria meningitidis*--drug effects--DE; *Penicillin Resistance--genetics--GE; Hexosyltransferases--genetics--GE; Hexosyltransferases--metabolism--ME; Meningitis, Meningococcal--microbiology--MI; Meningococcal Infections--microbiology--MI; Multienzyme Complexes--genetics--GE; Multienzyme Complexes--metabolism--ME; *Neisseria meningitidis*--classification--CL; *Neisseria meningitidis*--genetics--GE; Peptidyltransferase--genetics--GE; Peptidyltransferase--metabolism--ME; Spain--epidemiology--EP; beta-Lactamases--biosynthesis--BI; beta-Lactamases--genetics--GE

CAS Registry No.: 0 (Multienzyme Complexes); 9042-06-2 (peptidoglycan synthetase)

Enzyme No.: EC 2.3.2.12 (Peptidyltransferase); EC 2.4.1.- (Hexosyltransferases); EC 3.5.2.6 (beta-Lactamases)

Gene Symbol: penA

Record Date Created: 19920507

Record Date Completed: 19920507

6/9/9 (Item 9 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07299344 92162276 PMID: 1536720

Regulation of aspartate carbamoyltransferase in *Neisseria* and *Branhamella* species.

Jyssum S

Kaptein W. Wilhelmsen og Frues Bakteriologiske Institutt, University of Oslo, Rikshospitalet, Norway.

APMIS - acta pathologica, microbiologica, et immunologica Scandinavica (DENMARK) Jan 1992, 100 (1) p48-56, ISSN 0903-4641 Journal Code: 8803400

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The regulatory characteristics of aspartate carbamoyltransferase (ACTase EC 2.1.3.2) from various species of *Neisseria* and *Branhamella* have been compared. Great differences in the regulatory nature of the enzymes were observed. ATP and GTP were positive effectors in *Neisseria meningitidis*, *N. gonorrhoeae* and nine other coccal "true neisseriae" species. In four "false neisseriae" species, including *Branhamella catarrhalis*, no stimulating effect of ATP or GTP was observed. The rod-shaped *N. elongata* behaved as the "false neisseriae" in these respects, despite its taxonomic affinity to the coccal "true neisseriae" species. Except in *N. meningitidis* and *N. lactamica*, CTP had no distinct stimulatory effect. CTP had a strong inhibitory effect on ACTases from *N. elongata* and the "false neisseriae" species *N. caviae* and *B. catarrhalis*. The inhibitory effect of CTP was weak in *N. cinerea*, *N. denitrificans*, and the "false neisseriae" species *N. ovis* and *N. cuniculi*. Thus, there was no sharp reflection of taxonomy in the regulation of ACTase by CTP in these groups of bacteria. The apparent [S]_{0.5} values for aspartate and carbamoyl phosphate, displayed for five of the eighteen species, showed great variability with [S]_{0.5} values for aspartate ranging from 6 to 34, and for carbamoyl phosphate from 2 to 9. Treatment of the enzyme from the main test microbe *N. meningitidis* strain M1 by heat or para-chloromercuribenzoate (pCMB) showed that both the catalytic and the regulatory functions decreased in parallel as in the class A enzymes found in species of *Pseudomonas*. An estimation of the molecular weight (Mr) of the ACTase enzyme from *N. meningitidis* showed it to be about 295,000, which resembles the class B enzymes found in the Enterobacteriaceae.

Tags: Comparative Study

Descriptors: *Aspartate Carbamoyltransferase--metabolism--ME; *Moraxella--enzymology--EN; *Neisseria--enzymology--EN; Aspartate Carbamoyltransferase--chemistry--CH; Aspartic Acid--metabolism--ME; Carbamyl Phosphate--metabolism--ME; Chloromercuribenzoates--chemistry--CH; Enzyme Activation; Heat; Molecular Weight; Nucleotides--pharmacology--PD; p-Chloromercuribenzoic Acid

CAS Registry No.: 0 (Chloromercuribenzoates); 0 (Nucleotides); 56-84-8 (Aspartic Acid); 59-85-8 (p-Chloromercuribenzoic Acid); 590-55-6 (Carbamyl Phosphate)

Enzyme No.: EC 2.1.3.2 (Aspartate Carbamoyltransferase)

Record Date Created: 19920331

Record Date Completed: 19920331

6/9/10 (Item 10 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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06917986 91158313 PMID: 2127349

Neisseria lactamica and *Neisseria polysaccharea* as possible sources of meningococcal beta-lactam resistance by genetic transformation.

Saez-Nieto J A; Lujan R; Martinez-Suarez J V; Berron S; Vazquez J A; Vinas M; Campos J

Laboratorio de Referencia de Meningococos, Centro Nacional de Microbiologia, Madrid, Spain.

Antimicrobial agents and chemotherapy (UNITED STATES) Nov 1990, 34 (11) p2269-72, ISSN 0066-4804 Journal Code: 0315061

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We studied the susceptibilities of relatively penicillin G-resistant and

-susceptible strains of *Neisseria meningitidis*, as well as *Neisseria lactamica* and *Neisseria polysaccharea*, to penicillin, ampicillin, and several cephalosporins. The MICs of penicillin, ampicillin, cephalothin, and cefuroxime for moderately resistant meningococci have increased two- to sixfold in relation to MICs for susceptible strains. For these strains of meningococci, *N. lactamica*, and *N. polysaccharea*, penicillin, ampicillin, cephalothin, and cefuroxime MICs for 50 and 90% of strains were similar. By genetic transformation of a penicillin-susceptible strain of *N. meningitidis* to low-level penicillin resistance with DNA from penicillin-resistant strains of *N. meningitidis*, *N. lactamica*, *N. polysaccharea*, and *N. gonorrhoeae*, isogenic strains with the same pattern of resistance to beta-lactams were obtained, suggesting that these commensal *Neisseria* spp. could be the source of meningococcal resistance genes.

Tags: Support, Non-U.S. Gov't

Descriptors: *Antibiotics, Lactam--pharmacology--PD; *Drug Resistance, Microbial--genetics--GE; *Neisseria--genetics--GE; *Neisseria meningitidis--genetics--GE; DNA, Bacterial--genetics--GE; DNA, Bacterial--isolation and purification--IP; Penicillin Resistance--genetics--GE; Phenotype; Transformation, Genetic

CAS Registry No.: 0 (Antibiotics, Lactam); 0 (DNA, Bacterial)

Record Date Created: 19910408

Record Date Completed: 19910408

6/9/11 (Item 11 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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06714030 90340048 PMID: 2116567

Distribution of gonococcal lipopolysaccharide biosynthesis genes among strains of *Neisseria gonorrhoeae* and other neisserial species.

Palermo-Dilts D A; Silver L E; Clark V L

Department of Microbiology and Immunology, School of Medicine and Dentistry, University of Rochester, NY 14642.

Microbial pathogenesis (ENGLAND) Mar 1990, 8 (3) p227-33, ISSN 0882-4010 Journal Code: 8606191

Contract/Grant No.: R01 AI 11709; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A plasmid, pTME6, containing *Neisseria gonorrhoeae* lipopolysaccharide biosynthesis genes was used as a probe to analyze DNA from strains of *N. gonorrhoeae*, *N. meningitidis* and various commensal *Neisseria* by Southern blotting. Chromosomal DNA from 26 gonococcal strains probed with 32P-labeled pTME6 produced five different hybridization patterns. No correlation between hybridization pattern and auxotype, serotype, serum sensitivity or SDS-urea-PAGE migration of LPS was observed. DNA from strains of *N. meningitidis*, *N. lactamica* and *N. cinerea*, but not other commensal *Neisseria* species, hybridized strongly to pTME6.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: DNA, Bacterial--genetics--GE; *Genes, Bacterial; *Lipopolysaccharides--genetics--GE; *Neisseria--genetics--GE; *Neisseria gonorrhoeae--genetics--GE; *Streptococcus--genetics--GE; Lipopolysaccharide s--biosynthesis--BI; *Neisseria gonorrhoeae*--growth and development--GD; Nucleic Acid Hybridization; Restriction Mapping; Streptococcus--growth and development--GD

CAS Registry No.: 0 (DNA, Bacterial); 0 (Lipopolysaccharides)

Record Date Created: 19900912

Record Date Completed: 19900912

6/9/12 (Item 12 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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06560016 90185237 PMID: 2155857

DNA methylation in *Neisseria gonorrhoeae* and other *Neisseriae*.

Ritchot N; Roy P H

Departement de Biochimie, Faculte des Sciences et de Genie, Universite Laval, Sainte-Foy, Canada.

Gene (NETHERLANDS) Jan 31 1990, 86 (1) p103-6, ISSN 0378-1119

Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

It has been reported in the literature that *Neisseria gonorrhoeae* DNA is modified by the methyltransferases (MTases) M.NgoI, M.NgoII, and M.NgoIII, as well as three other cytosine MTases and one adenine MTase, even if the corresponding restriction endonucleases are not present. We envisioned the possibility of cloning one of the *N. gonorrhoeae* MTase-encoding genes for use as a species-specific DNA probe. We therefore undertook a survey of methylation patterns of several clinical isolates of *N. gonorrhoeae* and *N. meningitidis* as well as ATCC strains of other *Neisseriae*. We found, from digestion patterns with isoschizomers, one *N. gonorrhoeae* strain that lacked M.NgoII and two that lacked M.NgoIII. All *N. meningitidis* strains (save one) were resistant to digestion with NlaIV thus possessing an MTase like NgoV, and one was resistant to SstII, thus having an NgoIII-like MTase. None were resistant to isoschizomers of NgoI, NgoIII and NgoIV. Some other *Neisseriae* had an MTase with NlaIV (NgoV) specificity, but none had NgoI, II, III or IV specificity, except for the Branhamella-like *N. caviae*-*ovis* group and *N. lactamica* where these specificities were present in at least one strain of this group. Therefore, among the *Neisseriae* other than *N. caviae* only M.NgoI is *N. gonorrhoeae*-specific.

Descriptors: DNA Modification Methylases--metabolism--ME; **Neisseria* --genetics--GE; **Neisseria gonorrhoeae*--genetics--GE; DNA Restriction Enzymes--metabolism--ME; DNA, Bacterial--metabolism--ME; Methylation; *Neisseria*--enzymology--EN; *Neisseria gonorrhoeae*--enzymology--EN

CAS Registry No.: 0 (DNA, Bacterial)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19900426

Record Date Completed: 19900426

6/9/13 (Item 13 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05906542 88260884 PMID: 2455211

Common mechanism controlling phase and antigenic variation in pathogenic *neisseriae*.

Stern A; Meyer T F

Max-Planck-Institut fur Biologie, Infektgenetik, Tubingen, FRG.

Molecular microbiology (ENGLAND) Jul 1987, 1 (1) p5-12, ISSN

0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The expression of the *Neisseria gonorrhoeae* opacity protein (Op, protein II), a major antigenic determinant of the outer membrane, is subject to frequent phase transitions. At least nine expression loci (opaE) are involved in the production of a large number of serologically distinct Op types. Using opa-specific oligonucleotides as probes in genomic blots, we detect Op-related gene sequences (opr) in *N. meningitidis* as well as in *N. lactamica*. DNA sequence analysis of such opr genes derived from *N. meningitidis* reveals distinct regions of homology with gonococcal opa E genes. As shown in the immunoblot, the proteins encoded by opa and opr are serologically related. Like the opaE genes, the 5'-coding sequences of the opr genes include a repetitive sequence composed of pentameric CTCTT units. The number of these coding repeat (CR) units is variable. This

finding, together with the observation that all opr genes are constitutively transcribed, regardless of the status of protein production, suggests a translational control mechanism identical to that of the opa genes in gonococci. The related structures and control mechanisms of opa and opr genes imply a general significance of their gene products for the pathogenic character of the investigated Neisseria species.

Tags: Support, Non-U.S. Gov't

Descriptors: *Antigens, Bacterial--genetics--GE; *Bacterial Outer Membrane Proteins--genetics--GE; *Genes, Bacterial; *Genes, Structural; *Neisseria--genetics--GE; Amino Acid Sequence; Antigens, Bacterial--immunology--IM; Base Sequence; Epitopes--genetics--GE; Molecular Sequence Data; Neisseria gonorrhoeae--genetics--GE; Neisseria meningitidis--genetics--GE; Species Specificity

Molecular Sequence Databank No.: GENBANK/X06445; GENBANK/X06446

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Outer Membrane Proteins); 0 (Epitopes); 0 (opacity protein (Neisseria gonorrhoeae))

Record Date Created: 19880811

Record Date Completed: 19880811

6/9/14 (Item 14 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

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05724081 88077454 PMID: 3120761

Deoxyribonucleic acid relatedness among Neisseria gonorrhoeae, N. meningitidis, N. lactamica, N. cinerea and "Neisseria polysaccharea".

Guibourdenche M; Popoff M Y; Riou J Y

Laboratoire des Neisseria, Institut Pasteur, Paris.

Annales de l'Institut Pasteur. Microbiology (FRANCE) Sep-Oct 1986, 137B (2) p177-85, ISSN 0769-2609 Journal Code: 8701984

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Deoxyribonucleic acid relatedness studies (S1 nuclease method with DE-81 filters method) indicated that Neisseria gonorrhoeae, N. meningitidis, N. lactamica and "N. polysaccharea" form a single genospecies, in which four subspecies can be delineated. However, from a clinical and practical viewpoint, it seems desirable to maintain N. gonorrhoeae, N. meningitidis, N. lactamica and "N. polysaccharea" as separate species. N. cinerea is a valid species, closely related to N. gonorrhoeae, N. meningitidis, N. lactamica and "N. polysaccharea". These five species were 0 to 46% related to the other known species of the genus Neisseria.

Tags: Comparative Study

Descriptors: DNA, Bacterial; *Neisseria--classification--CL; Neisseria--genetics--GE; Neisseria gonorrhoeae--classification--CL; Neisseria gonorrhoeae--genetics--GE; Neisseria meningitidis--classification--CL; Neisseria meningitidis--genetics--GE; Nucleic Acid Hybridization

CAS Registry No.: 0 (DNA, Bacterial)

Record Date Created: 19880126

Record Date Completed: 19880126

6/9/15 (Item 15 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

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05485698 87164490 PMID: 2881892

Distribution of specific DNA sequences among pathogenic and commensal Neisseria species.

Aho E L; Murphy G L; Cannon J G

Infection and immunity (UNITED STATES)

ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: AI15036; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Apr 1987, 35 (4) p1009-13,

Record type: Completed

Subfile: INDEX MEDICUS

Several traits, including pili and the outer membrane proteins P.II and H.8, have been associated with pathogenic *Neisseria* species. We examined several *Neisseria* species for DNA sequence homology to cloned pilin, P.II, and H.8 genes. Strains of *Neisseria gonorrhoeae* and *N. meningitidis* showed hybridization to all of these genes. Commensal strains showed little hybridization to any of these genes. Strains of *N. lactamica* and *N. cinerea* showed intermediate patterns of hybridization. Generally, organisms that expressed a given trait showed DNA homology to the corresponding cloned gene. However, we observed pili on some commensal strains that did not show hybridization to the cloned gonococcal pilin gene.

Tags: Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Outer Membrane Proteins--genetics--GE; **Neisseria* --genetics--GE; Fimbriae Proteins; Fimbriae, Bacterial; Genes, Structural; *Neisseria*--pathogenicity--PY; *Neisseria gonorrhoeae*--genetics--GE; *Neisseria meningitidis*--genetics--GE; Nucleic Acid Hybridization; Sequence Homology, Nucleic Acid

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 147680-16-8 (Fimbriae Proteins)

Record Date Created: 19870430

Record Date Completed: 19870430

6/9/16 (Item 16 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05379832 87058180 PMID: 3097079

Homology of cryptic plasmid of *Neisseria gonorrhoeae* with plasmids from *Neisseria meningitidis* and *Neisseria lactamica*.

Ison C A; Bellinger C M; Walker J

Journal of clinical pathology (ENGLAND) Oct 1986, 39 (10) p1119-23, ISSN 0021-9746 Journal Code: 0376601

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

DNA probe hybridisation was used to examine the relation between the cryptic plasmid from *Neisseria gonorrhoeae* and plasmids carried by pharyngeal isolates of *Neisseria meningitidis* and *Neisseria lactamica*. The complete gonococcal cryptic plasmid and *Hinf*I derived digestion fragments subcloned into *Escherichia coli* were used to probe Southern blots of plasmid extracts. Homology was found to a plasmid of approximate molecular weight 4.5 kilobase pairs (Kb) but not to plasmids of less than 3.2 Kb or 6.5 Kb. Eleven of 16 strains of *N. meningitidis* and two of six strains of *N. lactamica* carried plasmids that showed strong hybridisation with the 4.2 Kb gonococcal plasmid. Hybridisation of plasmids from non-gonococcal species of *Neisseria* with the gonococcal cryptic plasmid indicates that caution should be taken when using the cryptic plasmid as a diagnostic probe for gonorrhoea.

Descriptors: **Neisseria*--genetics--GE; *Plasmids; DNA, Bacterial; Electrophoresis, Agar Gel; Molecular Weight; *Neisseria*--classification--CL; *Neisseria gonorrhoeae*--genetics--GE; *Neisseria meningitidis*--genetics--GE; Nucleic Acid Hybridization

CAS Registry No.: 0 (DNA, Bacterial); 0 (Plasmids)

Record Date Created: 19870105

Record Date Completed: 19870105

6/9/17 (Item 17 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05101464 86101901 PMID: 3936398

[Enzymatic profile and plasmid content of *Neisseria polysacchareae*]

Profil enzymatique et contenu plasmidique de "*Neisseria polysacchareae*".

Delmas C; Prere M F; Fayet O; Lareng M B; Dabernat H
Annales de l'Institut Pasteur. Microbiologie (FRANCE) Jul-Aug 1985,
136B (1) p29-38, ISSN 0769-2609 Journal Code: 8503044

Document type: Journal Article ; English Abstract

Languages: FRENCH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The enzymatic profile of "Neisseria polysacchareae" was determined by using chromogenic substrate (API System), and was compared to that of *N. meningitidis*, *N. gonorrhoeae* and *N. lactamica*. The tested classes of enzymes were aminopeptidase, proteases, esterases, lipases, glycosidases, phosphatase and phosphoamidase. "*N. polysacchareae*" exhibited various aminopeptidase and protease activities and a strong esterase activity. No lipase and glycosidase activities were detected by the tested substrates. The strains of "*N. polysacchareae*" differed from that of *N. meningitidis* in the presence of hydroxyproline aminopeptidase and the lack of gamma-glutamyl-transferase activity. Five strains harboured extrachromosomal elements. The plasmids were of 4.2 Kb in size in four cases and of more than 40 Kb in four cases. Three strains simultaneously harboured these two plasmids. This plasmid content is another characteristic of strains of this new taxon. No phenotypic modification was observed in plasmid-containing strains.

Descriptors: *Neisseria--enzymology--EN; *Plasmids; DNA --analysis--AN; Electrophoresis, Agar Gel; Neisseria--classification--CL; Neisseria --genetics--GE; Neisseria gonorrhoeae--enzymology--EN; Neisseria meningitidis--enzymology--EN

CAS Registry No.: 0 (Plasmids); 9007-49-2 (DNA)

Record Date Created: 19860130

Record Date Completed: 19860130

6/9/18 (Item 18 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

05084041 86084472 PMID: 3941006

Distribution of an antigenically related iron-regulated protein among the *Neisseria* spp.

Mietzner T A; Barnes R C; JeanLouis Y A; Shafer W M; Morse S A

Infection and immunity (UNITED STATES) Jan 1986, 51 (1) p60-8,

ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: AI 13571; AI; NIAID; AI 22148; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Several iron-regulated proteins of *Neisseria gonorrhoeae* have been reported. One of these, a 37,000-molecular-weight protein (37K protein), appears to be common to all gonococcal isolates. Recently, the occurrence of a similar protein has also been noted in *N. meningitidis*. The gonococcal 37K protein has been purified and used to produce both rabbit monospecific antiserum and murine monoclonal antibodies. Using these antibody reagents, we analyzed 57 strains from nine species of *Neisseria* and the closely related organism *Branhamella catarrhalis* for the presence of proteins antigenically related to the gonococcal 37K protein. Strains grown on medium with low iron content were probed for antigenic reactivity by Western blot techniques and an enzyme-linked immunosorbent assay. Proteins which cross-reacted with the rabbit monospecific antiserum were designated as AgR-37K proteins. The data indicated that the AgR-37K proteins were conserved among the 40 strains of *N. gonorrhoeae*, *N. meningitidis*, *N. lactamica*, and *N. cinerea* tested. Seventeen strains from other species of *Neisseria* and *Branhamella* did not express AgR-37K proteins with the exception of one *N. subflava* isolate. All AgR-37K proteins appeared to be regulated by the amount of available iron in the growth medium. Murine monoclonal antibodies were used to probe the antigenic heterogeneity of the AgR-37K proteins from different *Neisseria* spp. Two of seven monoclonal antibodies were broadly cross-reactive,

recognizing the AgR-37K proteins from all species examined. The remaining five monoclonal antibodies were more discriminating, recognizing the AgR-37K proteins from certain species. The antigenic conservation of these AgR-37K proteins, particularly among the pathogenic members of the genus *Neisseria*, may imply that these proteins serve a common function in pathogenicity.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Proteins--metabolism--ME; *Membrane Proteins--metabolism--ME; *Neisseria--genetics--GE; Antibodies, Bacterial--immunology--IM; Antibodies, Monoclonal--immunology--IM; Antibody Specificity; Antigens, Bacterial--immunology--IM; Bacterial Proteins--genetics--GE; Bacterial Proteins--immunology--IM; Cross Reactions; Gene Expression Regulation; Iron--physiology--PH; Membrane Proteins--genetics--GE; Membrane Proteins--immunology--IM; Molecular Weight; Neisseria--immunology--IM; Species Specificity

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antibodies, Monoclonal); 0 (Antigens, Bacterial); 0 (Bacterial Proteins); 0 (Membrane Proteins); 7439-89-6 (Iron)

Record Date Created: 19860219

Record Date Completed: 19860219

6/9/19 (Item 19 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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04008551 83137285 PMID: 6219168

Differentiation of neisseriaceae by isoenzyme electrophoresis.

Braude A I; McCutchan J A; Ison C; Sargeant P R

Journal of infectious diseases (UNITED STATES) Feb 1983, 147 (2) p247-51, ISSN 0022-1899 Journal Code: 0413675

Contract/Grant No.: AI11643; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

Analysis of 71 strains of *Neisseriaceae* by starch-gel electrophoresis of hexokinase, phosphoglucosmutase, glucose phosphate isomerase, and L-malate-nicotinamide adenine dinucleotide phosphate oxidoreductase showed that all **gonococci** and all meningococci have a characteristic hexokinase isoenzyme that is specific for each species and clearly distinguishes meningococci and **gonococci** from each other and from other species of *Neisseriaceae*. Strains of **gonococci** that were transformed into maltose utilizers by DNA from *Neisseria lactamica* and *Neisseria meningitidis* showed no change in the isoenzymes so that they could still be differentiated from meningococci and other *Neisseriaceae* by isoenzyme electrophoresis. In view of the limited sensitivity and specificity of conventional tests for the identification of **gonococci** and the possibility that **gonococci** may be transformed into maltose utilizers by DNA from normal throat flora, electrophoresis of hexokinase isoenzymes should be useful for the precise laboratory identification of the pathogenic neisseriae, especially those from atypical sites and those giving indeterminate reactions.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *Isoenzymes--metabolism--ME; *Neisseria--classification--CL; Electrophoresis, Starch Gel; Glucose-6-Phosphate Isomerase--metabolism--ME; Hexokinase--metabolism--ME; Malate Dehydrogenase--metabolism--ME; Maltose--metabolism--ME; Neisseria--enzymology--EN; Neisseria--metabolism--ME; Phosphoglucosmutase--metabolism--ME; Transformation, Bacterial

CAS Registry No.: 0 (Isoenzymes); 69-79-4 (Maltose)

Enzyme No.: EC 1.1.1.37 (Malate Dehydrogenase); EC 2.7.1.1 (Hexokinase); EC 5.3.1.9 (Glucose-6-Phosphate Isomerase); EC 5.4.2.2 (Phosphoglucosmutase)

Record Date Created: 19830407

Record Date Completed: 19830407

6/9/20 (Item 20 from file: 155)

03903173 83031326 PMID: 6813359

Acquisition of new genes by oral Neisseria.

Ison C; Glynn A A; Bascomb S

Journal of clinical pathology (ENGLAND) Oct 1982, 35 (10) p1153-7,

ISSN 0021-9746 Journal Code: 0376601

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

It is suggested that part of the increased pharyngeal carriage of meningococci reported in patients with **gonorrhoea** is due to misidentification of **gonococci** which have been transformed to maltose fermenters by **DNA** from normal throat flora. The distribution of specific aminopeptidases in strains of **gonococci**, meningococci isolated from the throat and meningococci from systemic infections is consistent with this view. **Gonococci** oxidising maltose and **gonococci** with gamma-L-glutamyl aminopeptidase activity, both factors regarded as typical of *Neisseria meningitidis*, can be produced in vitro by transformation with **DNA** from *N. lactamica* and *N. meningitidis*. The clinical and theoretical implications of such changes are discussed.

Tags: Human; Male; Support, Non-U.S. Gov't

Descriptors: *Genes, Bacterial; *Neisseria gonorrhoeae--genetics--GE; *Neisseria meningitidis--genetics--GE; *Pharynx--microbiology--MI; Aminopeptidases--metabolism--ME; Asparaginase--metabolism--ME; Glutaminase--metabolism--ME; Microbial Sensitivity Tests; Neisseria gonorrhoeae--drug effects--DE; Neisseria meningitidis--drug effects--DE; Oleic Acids--pharmacology--PD; Phenotype; Transformation, Bacterial

CAS Registry No.: 0 (Oleic Acids)

Enzyme No.: EC 3.4.11 (Aminopeptidases); EC 3.5.1.1 (Asparaginase); EC 3.5.1.2 (Glutaminase)

Record Date Created: 19821221

Record Date Completed: 19821221

6/9/21 (Item 21 from file: 155)

03827668 82239743 PMID: 6808013

Laboratory diagnosis of gonococcal infection by genetic transformation.

Butler L O; Knight R D

Journal of clinical microbiology (UNITED STATES) May 1982, 15 (5) p810-4, ISSN 0095-1137 Journal Code: 7505564

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The transformation test for the detection of infection by *Neisseria gonorrhoeae* has been examined using pro **gonococci** as recipients and **DNA** preparations from 912 clinical isolates and from 240 direct swab specimens as donors. The reliability of the method was checked with **DNA** from clinical isolates; 82% of the *N. meningitidis* from throat swab specimens were capable of transforming the **gonococcal** recipients, but after identification of the meningococcus by the aminopeptidase profile, the transformation test was then 99.5% positive for the **gonococcus** with virtually no false-positives. The only other organism to give a positive reaction was *N. lactamica*, which occurred once in 912 specimens. When applied directly to swab specimens, the reliability of the test was reduced, but this may have been related to variability of the specimen itself. However, 7 of 15 specimens which were microscopically suspected to be **gonococci** but unculturable were positive; also, 9 out of 38 unculturable specimens that were not even suspected to be **gonococci** were positive. Hence the test was able to identify the presence of **gonococci** that were unculturable. The aminopeptidase activities were not sensitive

enough to be detected in the direct swab specimens, and neither cys nor leu auxotrophs were suitable as recipients to give a differentiation between *N. gonorrhoeae* and *N. meningitidis*. Evidence was obtained which would support the proposition that the transfer of genetic material between *N. gonorrhoeae* and *N. meningitidis* may occur.

Tags: Human; Support, Non-U.S. Gov't

Descriptors: *Bacteriological Techniques; *Gonorrhea--diagnosis--DI; *Transformation, Bacterial; Aminopeptidases--metabolism--ME; *Neisseria gonorrhoeae*--enzymology--EN; *Neisseria gonorrhoeae*--genetics--GE; *Neisseria meningitidis*--genetics--GE

Enzyme No.: EC 3.4.11 (Amino-peptidases)

Record Date Created: 19820910

Record Date Completed: 19820910

6/9/22 (Item 22 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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02179265 76133398 PMID: 814781

Radiorespirometric studies in genus *Neisseria*. 2. The catabolism of glutamate and fumarate.

Holten E

Acta pathologica et microbiologica Scandinavica. Section B, Microbiology (DENMARK) Feb 1976, 84 (1) p1-8, ISSN 0105-0656 Journal Code: 7508472

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The catabolism of glutamate and fumarate was studied by radiorespirometry in selected *Neisseria* species. The tricarboxylic acid cycle is functioning in all species tested, in spite of the known absence of in vitro malate dehydrogenase activity in *N. meningitidis*, *N. gonorrhoeae* and *N. cinerea*. The results imply a pyridine nucleotide independent oxidation of malate. The oxidation of glutamate is less complete in the presence of phosphate. In *N. meningitidis*, *N. perflava*, *N. flava*, *N. subflava* and *N. lactamica* the catabolism of fumarate was slow and incomplete in the absence of glutamate.

Descriptors: *Fumarates--metabolism--ME; *Glutamates--metabolism--ME; **Neisseria*--metabolism--ME; Carbon Dioxide--metabolism--ME; Citric Acid Cycle; Malate Dehydrogenase--metabolism--ME; *Neisseria*--enzymology--EN; *Neisseria gonorrhoeae*--metabolism--ME; *Neisseria meningitidis*--metabolism--ME

CAS Registry No.: 0 (Fumarates); 0 (Glutamates); 124-38-9 (Carbon Dioxide)

Enzyme No.: EC 1.1.1.37 (Malate Dehydrogenase)

Record Date Created: 19760409

Record Date Completed: 19760409

6/9/23 (Item 23 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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02117664 76069099 PMID: 811645

Intragenetic transformation of *neisseria gonorrhoeae* and *neisseria perflava* to streptomycin resistance and nutritional independence.

Siddiqui A; Goldberg I D

Journal of bacteriology (UNITED STATES) Dec 1975, 124 (3) p1359-65, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Auxotrophic mutants of *Neisseria gonorrhoeae* and *Neisseria perflava* were transformed to prototrophy using homologous and heterologous

deoxyribonucleic acid (DNA). Within either species the efficiencies of transformation for nutritional markers were found to be very similar to the values obtained for transformation to streptomycin resistance. The number of transformants in the interspecific *N. perflava* (donor) - - leads to *N. gonorrhoeae* (recipient) cross was 100-fold lower than the number obtained in the intraspecific *N. gonorrhoeae* - - leads to *N. gonorrhoeae* cross for streptomycin resistance, as well as for several nutritional markers. In the reciprocal experiment the difference in the number of transformants in the interspecific *N. gonorrhoeae* - - leads to *N. perflava* cross and the number obtained in the intraspecific *N. perflava* - - leads to *N. perflava* cross varied from 600 to 1,000-fold for the streptomycin resistance marker. Of greater interest was the finding that *N. perflava* auxotrophs, although transformable to prototrophy with wild-type *N. perflava* DNA , were not transformed to nutritional independence by gonococcal DNA . These same mutants were transformable to streptomycin resistance using the heterologous gonococcal DNA . When the DNAs of *N. meningitidis* , *N. flava*, and *N. lactamicus* were used to transform *N. gonorrhoeae* to prototrophy or streptomycin resistance, the transformation frequencies obtained fell along a gradient that in general reflected taxonomic relationships. On the other hand, with *N. perflava* as the recipient for these same DNAs, only *N. flava* DNA could transform auxotrophs to prototrophy, although transformation to streptomycin resistance occurred in all cases. DNA from *N. perflava* - - leads to *N. gonorrhoeae* streptomycin-resistant or Ade+ intergenetic transformants transformed *N. gonorrhoeae* cells at a 100-fold-higher efficiency than did DNA from *N. perflava*. Our findings suggest that (i) *N. gonorrhoeae* and *N. perflava* are more closely related than hitherto suspected and (ii) *N. perflava* is more selective with respect to heterologous DNA than is *N. gonorrhoeae*.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Neisseria; *Neisseria gonorrhoeae; *Transformation, Genetic ; Amino Acids--metabolism--ME; DNA , Bacterial; Drug Resistance, Microbial ; Mutation; Neisseria--drug effects--DE; Neisseria--metabolism--ME; Neisseria gonorrhoeae--drug effects--DE; Neisseria gonorrhoeae--metabolism--ME; Species Specificity; Streptomycin--pharmacology--PD

CAS Registry No.: 0 (Amino Acids); 0 (DNA, Bacterial); 57-92-1 (Streptomycin)

Record Date Created: 19760220

Record Date Completed: 19760220

6/9/54 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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0005561335 BIOSIS NO.: 198783040226

DNA RELATEDNESS AMONG NEISSERIA- GONORRHOEAE NEISSERIA- MENINGITIDIS
NEISSERIA- LACTAMICA NEISSERIA-CINEREA AND NEISSERIA-POLYSACCHAREA

AUTHOR: GUIBOURDENCHE M (Reprint); POPOFF M Y; RIOU J Y

AUTHOR ADDRESS: LAB NEISSERIA, UNITE D'ECOLOGIE BACTERIENNE, INST PASTEUR,
75724 PARIS CEDEX 15, FR**FRANCE

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ISSN: 0769-2609

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Deoxyribonucleic acid relatedness studies (S1 nuclease method with DE-81 filters method) indicated that *Neisseria gonorrhoeae* , *N. meningitidis* , *N. lactamica* and "*N. polysaccharea*" form a single genospecies, in which four subspecies can be delineated. However, from a clinical and practical viewpoint, it seems desirable to maintain *N. gonorrhoeae* , *N. meningitidis* , *N. lactamica* and "*N. polysaccharea*" as separate species. *N. cinerea* is a valid species, closely related to *N. gonorrhoeae* , *N. meningitidis* , *N. lactamica* and "*N. polysaccharea*". These five species were 0 to 46 % related to the other known species of the genus *Neisseria*.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics;
 Infection; Physiology; Systematics and Taxonomy
 BIOSYSTEMATIC NAMES: Neisseriaceae--Gram-Negative Aerobic Rods and Cocci,
 Eubacteria, Bacteria, Microorganisms
 COMMON TAXONOMIC TERMS: Bacteria; Eubacteria; Microorganisms
 CONCEPT CODES:
 00504 General biology - Taxonomy, nomenclature and terminology
 10010 Comparative biochemistry
 10062 Biochemistry studies - Nucleic acids, purines and pyrimidines
 30000 Bacteriology, general and systematic
 31000 Physiology and biochemistry of bacteria
 31500 Genetics of bacteria and viruses
 36002 Medical and clinical microbiology - Bacteriology
 BIOSYSTEMATIC CODES:
 06507 Neisseriaceae
 ?t s6/3,kwic/24-49 66 69 77 78 88 97

6/3,KWIC/24 (Item 1 from file: 654)
 DIALOG(R)File 654:US Pat.Full.
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 Derwent Accession: 1995-115461
Utility
 C/ Oligonucleotides and methods for the detection of *Neisseria gonorrhoeae*
 Inventor: Birkenmeyer, Larry G., Chicago, IL
 Ching, Shanfun, Libertyville, IL
 Ohhashi, Yoshihiro, Gurnee, IL
 Winkler, Janet K., Lindenhurst, IL
 Assignee: Abbott Laboratories (02), Abbott Park, IL
 Abbott Laboratories (Code: 00152)
 Examiner: Parr, Margaret (Art Unit: 187)
 Assistant Examiner: Horlick, Kenneth R.
 Combined Principal Attorneys: Brainard, Thomas D.; Yasger, Paul D.

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